GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 26, 2005, 03:47:51; Search time 211 Seconds (without alignments) 7816.905 Million cell updates/sec Run on:

1 ggagtggaatcagtgagagg......gtaaaaaagataataagtaa 1008 US-10-724-972A-2580 1008 Title: Perfect score: Sequence:

1202784 seqs, 818138359 residues IDENTITY NUC | Gapoxt 1.0 Scoring table:

Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:*

1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 355, App	Sequence 355, App	255			604,	Sequence 604, App	15,	15,	Sequence 238, App	238,	3782,	2690,	383,	383	1357	37, 1	937, A	1583,	2208	-	39,	3348	4042,	3564,	Sequence 461, App	1267.
	OI.	US-08-956-171E-355	US-08-781-986A-355	US-08-956-171E-2556	US-08-781-986A-2556	US-09-134-001C-2023	US-08-956-171E-604	US-08-781-986A-604	US-09-830-217-15	US-10-278-946-15	US-08-956-171E-238	US-08-781-986A-238	US-09-710-279-3782	US-09-543-681A-2690	US-08-956-171E-383	US-08-781-986A-383	US-09-902-540-1357	US-09-071-035-37	US-09-134-000C-937	US-09-902-540-1583	US-09-902-540-2208	US-08-232-463-14	US-09-071-035-39	US-09-710-279-3348	US-09-710-279-4042	US-09-710-279-3564	US-09-710-279-461	736-016-016-011
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de	Query	22.1	22.1	16.1	16.1	15.7	12.4	12.4	12.3	12.3	12.3	12.3	10.9	7.7	7.3	7.3	7.2	7.0	7.0	6.9	6.8	6.8	6.5	6.4	6.4	6.4	6.4	•
	Score	222.6	222.6	162.2	162.2	158.2	125.4	125.4	124	124	124	124	109.4	77.2	73.8	73.8	72.2	70.6	70.6	69.8	68.8	68.8	65.6	64.6	64.6	64.6	64.4	
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28 64.4 6.4 31 623.6 63.6 31 623.6 63.8 32 61.8 61.1 34 59.8 61.8 35 59.9 36 64 5.6 41 56.4 5.6 41 56.4 5.6 42 55.2 5.5 44 55.8 54 55.8 54 55.8 55.8 56.8 56.8 57.8 57.8 58.8 58.8 58.8 58.8 58.8 58	US-09-134-001C-2655 US-09-902-540-1280 US-09-806-708B-22	US-09-543-681A-1393 US-08-956-171E-37 US-08-781-986A-37	US-09-601-198-75 US-08-487-826B-13 US-09-790-988-1	US-09-601-198-66 US-09-949-016-14624	US-09-902-540-1318 US-08-916-421B-1 US-09-692-570-1	US-09-134-000C-3335 US-08-559-896B-1 US-09-351-794A-1	US-09-107-532A-862
28 64.4 6.4 31 623.6 63.6 31 623.6 63.8 32 61.8 61.1 34 59.8 61.8 35 59.9 36 64 5.6 41 56.4 5.6 41 56.4 5.6 42 55.2 5.5 44 55.8 54 55.8 54 55.8 55.8 56.8 56.8 57.8 57.8 58.8 58.8 58.8 58.8 58.8 58	W 4 4	4 4 4	404	44.	44	4 6 4	4
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ALIGNMENTS

RESULT 1 105-06-171E-355 106-956-171E-355 106-956-171E-355 Patent No. 659314 GENERAL INFORMATION: GENERAL INFORMATION: Patrick S. Dillon Craig A. Rosen Steven C. Barash Michael R. Fannon TITLE OF INVENTION: Staphylococcus aureus Polynuclectides NUMBER OF SEQUENCES: 5256 CORRESPONDENCES: 5256 CORNERSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue STREET: 9410 Key West Avenue COUNTRY: Mockville STREET: 9410 Key West Avenue STREET: 9410 Key West Avenue COUNTRY: WEADABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COUNTRY: USA CONTRY: HPS: Diskette, 3.50 inch, 1.4Mb storage COUNTRY: WEADABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: ACTIT TOWN SOFTHARE ASCIT TEAT COMPUTER: ACTIT TOWN APPLICATION NUMBER: 00/009.861 FILING DATE: January 5, 1997 ATTORNY/AGENT INFORMATION: REGISTRATION NUMBER: 00/709.861 FILING DATE: January 5, 1997 ATTORNY/AGENT INFORMATION: TELEPRAN: (301) 309-8439 INFORMATION FOR SEQ ID NO: 355: SEQUENCE CHARACTERISTICS: LENGTH: 666 base pairs TYPER INCLE CACID TYPER CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: STRANDENESS: ATTORNY/ACTION NUMBER: 00/701/90 SETANDENESS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: STREETS CACID CACID CACID CACID TO THE CACID CACID CACID CACID TO THE CA

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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GTTGAATGCAGTTAAAAATAATCGCGTGGATATTGTTGACCGTGATGTTTGGGCAAGATC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747 ACAAATGAACACTGAAACTTTATCTCCAAGTGAATCCTGAGCGTATGTTCATAATGACAAA
                                                                                                                                                      1 TITATTAGCACATCCAAACTATTCATATGTTGGACAATTTTTAAACGAACTAGGATTTAA
                                                                                                                                                                                                                                                    61 AATGCATTAAGTGACGATGTAACAAAGGTTTAAGTAAATATTTGAAAGGACCTTACTT
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                                                                                 Gaps
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                                         DB 4; Length 668;
                                                                                 Indels
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                                                                                 94;
                                       Score 222.6; DB 4
Pred. No. 8.3e-39;
0; Mismatches 94
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COMPUTER: HP Vectra 486/33
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-OCC-1997
CLASSIPICATION > CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2556, Application US/08956171E; Patent No. 6593114; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles Kunsch
Gil H. Choi
                                       Query Match 22.1%;
Best Local Similarity 74.8%;
Matches 279; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskel
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STATE: Maryland
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  US-08-781-986A-355
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US-08-781-986A-355
US-08-781-986A-355
US-08-781-986A-355
Sequence 355, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
CORRESPONDENCE ADDRESS: 5.255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
STATE: Maryland
                                                                                                                                                                                                                                                                                              121 ACAATTAGACACTGAACATTTAGCTGATTTAAATCCAGAGCGTATGATCATTATGACAGA 180
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  Length 668;
                                            94; Indels
  DB 4;
Score 222.6; DB 4
Pred. No. 8.3e-39;
0; Mismatches 94
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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REGISTRATION UNDBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INPORMATION:
TELEFONE: (301) 309-8514
INPORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
  22.1%;
74.8%;
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                        Best Local Similarity 74.8
Matches 279; Conservative
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CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-956-171E-604
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                                                                                                                                                                                                                                                                                                                                    268 CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2556, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
TILLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             388 AGACACAAAGGTATTTATAAAGACTTAAATTAAATTGCTCCTACGATTGAACTTGAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                          328 CAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAAT
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                          Score 162.2; DB 4; Length 242;
Pred. No. 6.4e-26;
0; Mismatches 50; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
         TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDBESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
                                                                                                                                                                                            Query Match
Best Local Similarity 79.3%;
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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CLASSIPTICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 T 448
                                                                                                                                                            US-08-956-171E-2556
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14-08
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 CCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
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                                                                                                                                                                                                                                                                          2 GATGCATTAGCAGCATTAGACGTTAAACCAGTTGGTATTGCTGATGGTAAGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 GATGCGTTAGTTTAGATGTTAAAACCTGTTGGGATAGCGGATGATAACAAAAAAT
                                                                                                                                                                                                                                                                                                                                 268 CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                328 CAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAAT
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                                                                                                                                      Length 242;
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                                                                                                                                    Score 162.2; DB 4;
Pred. No. 6.4e-26;
0; Mismatches 50;
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Pred. No. 4.3e-25;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2023, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 604, Application US/08956171E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus epidermidis US-09-134-001C-2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%;
                                                                                                                                           16.1%;
79.3%;
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Best Local Similarity 98.2
Matches 160; Conservative
LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                               Best Local Similarity 79.3
Matches 191; Conservative
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301 ATGAAGAACTTGCCAATATCAATCCAAAAGTTATGATTTTAGCCACTGACGGAAAAACGG 360
                                                                                                                                                             415 idahadahadcanadirirahdacdirdacdanahanadiddirdahardandaddarira 474
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Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATTATAATGCAAATATTGAAGCATTTAAAACAGTCGCTAAAGCAGTAGGCAAAGAAAAG
                                                                                                                        878 TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA
                                         318 CTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAAACGCTG
                                                                               361 ACAAAAA----TAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTAAAAGCTG
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Pred. No. 8.1e-18;
1; Mismatches 247; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,446
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ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.2
Matches 289; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
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US-08-781-986A-604
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                                                                                        Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTIONS: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 AAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATAAAAAAGAAATAA 577
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MEDIUM TYPE Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIPRACATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 125.4; DB 4; Length
Pred. No. 8.1e-18;
1; Mismatches 247; Indels
                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear seq ID NO: 604: US-08-956-171E-604
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INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
                                                                     Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2115 base pairs
  Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
12.4%;
Best Local Similarity 53.2%;
Matches 289; Conservative
                                                                                                                                                                                                                                                                           CITY: Rockville
STATE: Maryland
COUNTRY: USA
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267 TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
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                                                                                                                                                                                                                   318 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACGGGACTTAATTGTCGCGTCAAAAGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      623 CAGGITIGCTIGCICAICCAAGCAACTCTIAIGTIGGICAATICCTAAGICAACTAGGIT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAGATATTA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             743 ACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGA 802
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                                                                                                                                                                                 327 GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 GGAAAGAAAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAAGTAGCTGCATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 TCCGT----GCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGTGAAATCTTAAATG
TAGACACAAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
                                                                                                                                                                                                                                                                                                                    tagaaatgaaaagttacgatcaattatctaaaatcgcacc------Aacag
                                                                                                                                                                                                                                                                                                                                                                    TTTCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
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                                         198 reacerceretarcririaecrerraacereraeerecreraeaarcareaaaa
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; Sequence 15, Application US/10278946
; Patent No. 6821754
; GENERAL INFORMATION:
    APPLICAMT: Simpson et al.
    TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
    FILE REFERENCE: PB461USD1
    CURRENT PILING DATE: 2002-10-24
; PRIOR PILING DATE: 2001-04-24
; PRIOR PILING DATE: 1999-06199
; PRIOR PILING DATE: 1999-03-18
; PRIOR PILING DATE: 1998-03-18
; PRIOR PILING DATE: 1998-03-0
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1998-05-07
; PRIOR FILING DATE: 1998-05-07
; RUGHER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAACAAAGTTCTAACGAACCTTCACTA 834
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; ORGANISM: Staphylococcus aureus
US-10-278-946-15
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    ATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAA
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GENERAL INFORMATION: Staphylococcus aureus Genes and Polypeptides
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PB461PCT
CURRENT APPLICATION UNMBER: US/09/830,217
CURRENT FILING DATE: 1990-10-18
PRIOR APPLICATION NUMBER: G0/080,296
PRIOR PILING DATE: 1998-04-01
PRIOR PLILNG DATE: 1998-04-01
PRIOR PLILNG DATE: 1998-04-01
PRIOR PLILNG DATE: 1998-04-01
PRIOR PLILNG DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
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Pred. No. 1.4e-17;
0; Mismatches 380; Indels
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12:3%;
Best Local Similarity 50.7%;
Matches 412; Conservative
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US-09-830-217-15
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Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barnah
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
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Pred. No. 1.4e-17;
0; Mismatches 380; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTAAAATGCTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA
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                                                                                                                                                                                                                                                                                storage
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.3%; Score 124; DB 4; 50.7%; Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 238:
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Science
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/191,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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764 rccaactracarcraaagaaagcarrccarraargaacgcrgarcararrrraragraa 823
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AATTAAAATGCTTGTTGCTTACCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA 119
                                           TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
                                                                                  120 TTCAAATAAACAATCATCATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT 179
                                                                                                                                                                                                                                                      300 ACCGAAATTCGAATACATAAAAATGATTAAAAGATACTAAGATTGTAGGTCAAGAACC 359
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Patent No. 6703492

GENERAL INFORMATION: GAPHICALIAM JOHN

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US

CURRENT PILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR PILING DATE: 1999-11-09

NUMBER OF SEQ. ID NOS: 44772

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                          180 gégráchácháchtanangggnahacchánagciártrigirhacgcrartanaggragccac
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                                                                                                                                                                                                                                                                                                            267 TCGTATTATAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA
                                                                                                                                 147 AGGTACTACGAAAGTACCTAAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGT
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US-09-710-279-3782
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Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CCUNTRY: USA
           GTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATA 565
                                                                                                                                                                                 623 CAGGITIGCTIGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT 682
                                                                                                                                                                                                                   704 ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAGATATTA 763
                                                                                                                                                                                                                                                                                                                                                                                                     764 rccaáctrácarcráaagaáágcaírccarráargaácgcrágarcarárrirrirgiágraá 823
                                                  527 GGAAAGAAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAGTAGCTGCATTCC
                                                                                                 AAAAAGA----AATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTGCTAAAT
                                                                                                                                        587 AAAAAGATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTGTTAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124; DB 4; Length 37
Pred. No. 1.8e-17;
0; Mismatches 380; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   803 CAAACAAAGCAAGTTCTAACGAACCTTCACTA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            824 AATCAGATCCAAATGCGAAAGATGCTGCATTA 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
BEGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: 98248PP
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%;
nilarity 50.7%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-781-986A-238
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Best Local Simi
Matches 412;
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622

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SEQ ID NO 3782
LENGTH: 3046
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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                         TTTAGGTAAAGAAGAAGGTAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGA 560
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522 TATCGACAGCACACGCTTTATTGACAGCCTCACTGAGCGTACAACGACTTTAGGTCAAAT 581
                                                                                                                                       582 TITITGGIAAAGAAGAACAAGCIAAAAATTATTAGCTGACTTCAATAGCAAATTGATAC 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73.8; DB 4;
Pred. No. 7.1e-07;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PB248P1
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SEQUENCE DESCRIPTION: SEQ ID NO: 383:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLORAGE, TANDER ACT OF THE TELECOMPUNICATION INFORMER: 46,789
TELECOMPUNICATION INFORMATION:
TELEPHONE: (240) 314-124
TELEPAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 383, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 421 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%;
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                                                                                                                                                                                                                                                                                      642 GGTAAAAGCAAAAA 655
                                                                                                                                                                                                                    561 ATATAAAAAAGAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-956-171E-383/c
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APPLICANT: GARY BRETON

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR PILING DATE: 1999-04-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2765 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCCAAGTAATGTAATAAAA 2823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AAAATCATTAAGCCCACTGTTCTTATTGCTGTCTTCTCTGGTTATCGCAGGTTGTGATAA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 TAATAGTICAAGTAACTCAAGTAAAGAGTCATCAAAAAGATGGAGTTGAAATCAAGCACGA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 AGAAGGTACTACGAAAGTACCTAAACACCTAAAACGTGTTGTTGTTGTTGAGTATTCATT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 AAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 CCTACCTAAATTTCTAGAGAAATACACCAACGAAAATGAGTACATCAACGAAGGTGGCCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 TAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 GTTTGAACCAAACTACGAAAACTCAGTACTACTGCCCCTGATCTGATTTTAACGGGTAG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 TAATAGACACAAAGGTATTTATAAAGACTTAAATAAATTGCTCCTACGATTGAACTGAA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 TCAAGGCACCACTGAGATCCCTGCTCACCCACAAAAGTGGTTGTGATGAACATGGAAAC 284
                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AAAAATTTTAAGTGTAATTGGCTTATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAA
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                         OTHER INFORMATION: Description of Artificial Sequence: synthetic correct of the control of the control of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the correct of the c
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                                                                                                                                                                                                                                                                                                                                                            1 GGAGTGGAATCAGTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTAT
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                Score 109.4; DB 4
Pred. No. 2.4e-14;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2690, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                             10.9%;
ilarity 95.0%;
Conservative (
          ORGANISM: Artificial Sequence
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Matches 270, Conservative
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SEQ ID NO 2690
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 113; Conserva
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US-09-543-681A-2690
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127 GTTGAAATCAAGCACGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTGTT 186
                                                                                                                                                                                  US-08-781-986A-383/C

Sequence 383, Application US/08781986A

Sequence 383, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEB: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GAATCAGTGAGAGGTTTAAAAATTTTAAGTGTAATTGGCTTATTGTTTTGTTTTAATTGCA 66
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                                   85 ATTTCGGTAAAAGATGAAAATGGTACAGTAAAAGTACCTAAAAGATGCAAAACGTATCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INPORMATION:
TELEPAN: (301) 309-8514
INFORMATION FOR SEQ ID NO: 383:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 421 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 117; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                          187 GTTCTTGAG 195
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                                                                                                      Grarradad 17
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RESULT 16

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GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wigagand, Mococcus xanthus Genome Sequences and Uses Thereof TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849) B
FULE REFERENCE: 38-10(15849) B
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72.2; DB 4; Pred. No. 1.7e-06; 0; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(612)
COTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
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Sequence 1357, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/09071035 Patent No. 6448043
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Best Local Similarity 50.4%;
Matches 173; Conservative (
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                                                                                                                                                    APPLICANT: Goldman, Barry S.
                                                                                                    GENERAL INFORMATION:
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NAME/KEY: unsure
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7.0%; Score 70.6; DB 3; Length 975;
Best Local Similarity 48.8%; Pred. No. 4.1e-06;
Matches 317; Conservative 0; Mismatches 314; Indels 1
                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB369P2
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDENESS: double
SUFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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RESULT 18

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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS FILE REPERENCE: 032796-031
FILE REPERENCE: 032796-031
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
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48.8%; Pred. No. 4.1e-06;
tive 0; Mismatches 314; Indels 18;
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; Sequence 1583, Application US/09902540
; Patent No. 6833447
Sequence 937, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.88
Matches 317; Conservative
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: Myxococcus xanthus
    ; TYPE: DNA
; ORGANISM: Myxoc
US-09-902-540-2208
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 AGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATA 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AAATCCGCGGTTTGACCATATTAAAGGTCAGATGAAAGGCGTTAAAAGTGTGGGTACAGA 66
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)8
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 601-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
                    APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Greeven C.
APPLICANT: Slater, Greeven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10/15849)B
CURRENT APPLICATION NUMBER: 20/1-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 AATGCGACAAGAAAAGTATACGATCAGCTTAGTCAAATTGCTCCGACTGTATTCTCTGA
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Pred. No. 5.7e-06;
0; Mismatches 202; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2208, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.9%;
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2208
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US-09-902-540-2208
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                                                                                                                                                         1 AATCCGCGGTTTGACCATATTAAAGGTCAGATGAAAGGCGTTAAAAGTGTGGGTACAGAA
                                                                                                                                                                                                                   35 AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAAT
                                                                                                                                                                                                                                                                                                                     385 AATAGACACAAAGGTATTTATAAAGACTTAAATTAAAATTGCTCCTACGATTGAACTGAAA
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                                                                                                          265 AATCGTATTAAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGT
                                                      Gaps
                                                      6
  Length 702;
                                                      Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
Score 68.8; DB 4;
Pred. No. 9.4e-06;
0; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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REPERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
18-08-322-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
     Query Match
Best Local Similarity 49.8%;
Matches 209; Conservative
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FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSE: Foley & L
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us-10-724-972a-2580.rni

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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 98,992
TELECOMMUNICATION INPORMATION:
TELEPRAN: (301) 309-8504
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
LENGTH: 889 Dase pairs
LENGTH: 889 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.3%;
Matches 294; Conservative 0
ATTORNEY/AGENT INFORMATION:
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US-09-071-035-39
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Retent No. 6448043

GENERAL INFORMATION:
APPLICANT: GIl H. Choi
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 ATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAA 260
                                                                                                                                                                                                                                                                                                             261 AAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAAC 320
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                                                                                                                                                                                         Query Match

6.8%; Score 68.8; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 235; Mismatches 147; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 ATATAAAAAGAAATAACTATGGATAAAAATCAAAAGG 598
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ZIP: 20850

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

COMPUTER: HP Vectra 486/33

CORRATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/071,035 FILING DATE:
         TELEFAX: (703)683-4109
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: mucletc acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZGPT-F18
 (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: Maryland
COUNTRY: USA
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 TELEPHONE:
TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 CITITAGAIGITAAACCIGITGGGAIAGCGGAIGAIAACAAAAAAATCGIAITAITAAAC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 AAGAAATCAGTAAACTTAAACCAGATTTAATTATTACTGATAATAATAGACACAAAGGTA 400
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US-09-710-279-3348/C
US-09-710-270-3348, Application US/09710279
Sequence 3348, Application US/09710279
Sequence 3348, Application US/09710279
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPRENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.1 TACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTTCATTTGTTGATGCGTTAGTTG
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Score 65.6; DB 3; Length 889;
Pred. No. 4.8e-05;
0; Mismatches 284; Indels 18;
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                   1006 T 1006
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LENGTH: 3267
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                                                                                                                                                                             Gaps
                                                        ORGANISM: Artificial Sequence
PRATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-31348
                                                                                                                                                                            30;
                                                                                                                                                Length 3153;
                                                                                                                                             Query Match 6.4%; Score 64.6; DB 4; Length 3 Best Local Similarity 47.0%; Pred. No. 0.0001; Matches 452; Conservative 0; Mismatches 479; Indels
Patentin Ver.
                             3153
 SOFTWARE: Pate
SEQ ID NO 3348
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                                  agrigattichaaigaaacrigraaccarcaaaaaraigirtrtgaagcaagriggraaagaaaar 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIMMELY, MILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE REFERENCE: 903480US
CURRENT APPLICATION NUMBER: 05/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PALENTIN Ver. 2.1
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: nucleic acid sequence US-09-710-279-4042
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Best Local Similarity 47.0%; Pred. No. 0.0001;
Matches 452; Conservative 0; Mismatches 479; Indels 30;
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1551 ACGACAACTATCAAACTAATTGATTAAATGAAGTAGTAGAAAGTTGAAAATAA 1610
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352 AAACTTAAAACCAGATTTAA---TTATTGCTGATAATAGACACAAAGGTATTTATAAA 408
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: U5/09/710,279
CURRENT PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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                                                                         292 AAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGT
                                                                                                                      906 AAAGATGATAAGTATTAATACTGGAAATTTAAAAGAAGTGAACTTTGATAAAGTTGCA
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US-09-710-279-461
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                                                  ACTANAGACTTTANTANGANAGTANTGTNTTTÄTTGGTTANCGANGGTGANCTNTCANCG 1396
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     CCTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGA---T 291
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Patent No. 6703492

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REPRENENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3564
                                                                                                     TCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGTT
                                                                                                                                                     TITIGGACCAGGAGGAAGATTIGGTGGTTTAGTGTTTGATACATTAGGATTTAAACCTGCA
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6.4%; Score 64.6; DB 4; Length 3618;
Best Local Similarity 47.0%; Pred. No. 0.00011;
Matches 452; Conservative 0; Mismatches 479; Indels 30;
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US-09-710-279-3564
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
                                                                                                                     30;
                                                                                  Length 1044;
                                                                                                                     Indels
                                                                                  Query Match 6.4%; Score 64.4; DB 4; 1
Best Local Similarity 47.1%; Pred. No. 9e-05;
Matches 450; Conservative 0; Mismatches 476;
                                                     US-09-710-279-461
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                                    Sequence 1267, Application US/09710279
; Sequence 1267, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND
FILE REPREBRUCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE PATENTING OF 2.1
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6.4%; Score 64.4; DB 4; Length 10%
Best Local Similarity 47.1%; Pred. No. 9e-05;
Matches 450; Conservative 0; Mismatches 476; Indels
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RESULT 27
US-09-710-279-1267
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472 GAATTTAAAAAAGCTGCACCAAAAGCTAAAGTTGTATATGTAGGTACAAGTGATGACAAC 531
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hiddle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANTION UNMER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
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                                         AATATTGATGCTTTTAAAACAATTTCAAAAGCTTTTAGGTAAAGAAGAAGAAGGTAAAAAA
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48.1%; Pred. No. 0.00013;
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; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1280
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SEQ ID NO 1280
LENGTH: 1039
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Matches 177; Conservative
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US-09-902-540-1280
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2655
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      GACAAAAAGGTTAGCAAAAGCCCGCATGGTC----AAAATATAAATAATATATT
                                                                                AACAAGCAGAATCCAGATGTTATTTTAGCTATGGATCGTGGTTCAGTTGTAGGTGGTAAA
                                                                                                                                                              CCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAAACGCTGTGAAAAAT
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Pred. No. 9e-05;
0; Mismatches 476; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2655, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus epidermidis US-09-134-001C-2655
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Best Local Similarity 47.1%;
Matches 450; Conservative (
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SEQUENCES RELATING TO PROTEUS MIRABIT
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310 TCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTA 369
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                                                                                                                                                                                                                                                  489
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                                                              KTWMNTWYWDMMTTMBTTTTTRNMTTSTNMTNNNNNMWAACTNNNNNMWKAYYAHATNNW
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Pred. No. 0.00029;
0; Mismatches 250; Indels
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Sequence 1939, Application US/09543681A
Sequence 10605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
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Best Local Similarity 47.1%;
Matches 225; Conservative
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SEQ ID NO 1393
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                                                                                                                                                                                                                                                                                                                       TTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 Taaaaaaaaaaaaaagtaaaatacataattiaaaaaacaaaaaacuccgcataaa 627
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                                                                 494 CAAAAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
                                                                                                                                TTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGA
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR PPLICATION NUMBER: US 60/147,133
PRIOR PILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
LENGTH, 1141
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Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFRMATION:
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US-08-781-986A-37

Sequence 37, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCGACGAAACCCGAAGTAATCTTTATCTCTGGACGTACAGCTAATCAAAAGAATTTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 AGATAAAGCTAAAGAATTAAATAAAGATTTAGATAACAAAATTGCTTCAATGAAAGATAA
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                                                                                                                                                                                                                                                                                                                                                                 TAAAGATGATAAATATACAAACGTTGGTAATTTAAAAGAAGTGAATTTTGATAAATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                 351 TAAACTTAAACCAGATTTAA---TTATTGCTGATAATAATAGACACAAAGGTATTTATAA
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                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                              Length 9834;
                                                                                                                                                                                                                            Score 61.8; DB 4;
Pred. No. 0.00052;
0; Mismatches 362;
                                                                                                                                                          37:
                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
            INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9834 base pairs
                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                              6.1%;
                                                                                                                                                                                                                                               Best_Local Similarity 47.0
Matches 334; Conservative
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US-08-956-171E-37
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APPLICANT: Charles Kunsch
G11 H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTIONS: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
                                                                                           215
                                                                                                                                                                                  TAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAA 335
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                                 TAATCAAATTGTTGAACAGCAAAATGATAAAGTTGTTATCAAGCACCTATTAGGTGAAAC
TAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTAC
                                                                                           GAAAGTACCTAAACACCCCTAAACGTGTTGTTCTTGAGTATTCATTTGTTGATGCGTT
                                                                                                                                     177 TGCAĞTATCTAAAATCCGTCTAAGGTTĞTACTGTTTĞATTTTGGTCTATATGACTCTTT
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MEDIUM TYPE: Dishette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciences, Inc
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APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-cc-1997
CLASTICATION: <URNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: January 5, 1996
APPLICATION WUBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Scie:
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08956171E Patent No. 6593114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
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US-08-956-171E-37
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AAAAATTAATGGTATTCATACAGAAGTTGTTCAAGATAAATATGGTAAAAATACATATAA 3794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UREALYTICUM
FILE OF INVENTION: UREALYTICUM
FILE REPERENCE: UAB-13452/22
CURRENT FALING DATE: 200-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
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TAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAA
                                                                                                      TCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTC
                                                                                                                                                                                                                                         679 TACAATTAAACAAATTGAGGAACTTGATAAAGTTGTAAAATAATTTTAAAA 729
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Best Local Similarity 44.4%;
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 181
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
US-09-601-198-75/c
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                                                                                                                                                 ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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Pred. No. 0.00052
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ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9834 base pairs
                     : 9410 Key West Avenue
Rockville
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Best Local Similarity 47.0%;
Matches 334; Conservative (
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STRANDEDNESS: double
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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49.6%; Pred. No.
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                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09790988; Patent No. 6632935; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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APPLICANT: Wellems, Thomas B.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Mattern C.
STORES
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Pred. No. 0.0024;
0; Mismatches 170; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 620 Newport Center Drive 16th Ploor
CITY: Newport Beach
STATE: California
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NAME: Igraelsen, Ned
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                        Sequence 13, Application US/08487826B Patent No. S993827
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.1%;
Matches 173; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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MOLECULE TYPE:
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US-08-487-826B-13
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US-08-487-826B-13
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                                                                                                                              15748 ATAAAATAAAAAAATTAAAAAATGTTAAAAAAAAAAATATATACATAAAAAAA
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APPLICANT: WATAANBE, HIDEMI
APPLICANT: WATAANBE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
TITLEONT: HATTORI, YOSHIYUKI
TITLE OF INVENTION GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR PRILIKG DATE: 2000-04-07
                                                                                                                                                                                                                                                                15868 AAATAAAAAATTTAATTAAATAAAAAAATTAAAAAATTTAA 15912
                                                                                                                                                                                                  550 AAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAA 594
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US-09-902-540-1318
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UNCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: URBALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT PILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR APPLICATION NUMBER: 60/073,189
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 66
LENGTH: 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 ATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTT 310
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Pred. No. 0.0014;
0; Mismatches 277; Indels
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8.09-999-016-14624/c
; Sequence 14624, Application US/09949016
; Patent No. 6812339
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US-09-601-198-66
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Best Local Similarity 44.8%;
Matches 225; Conservative
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APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Wyxococus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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LOCATION: (1)..(614)
OTHER INFORMATION: unsure at all n locations
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-100-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ TRANS. FASESEQ for Windows Version 4.0
SEQ ID NO 14624
LENGTH: 147382
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14624
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Best Local Similarity 48.2%;
Matches 193; Conservative (
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APPLICANT: Goldman, Barry S.
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LOCATION: (1)...(14738;
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LOCATION: (319226). (319226)
OCHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (559167). (559167)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (559241). (559241)
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ION: (103998)..(103998)
INFORMATION: n equals a,
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NAME/KEY: mlsc feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a,
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DTHER INFORMATION: n equals a,
NAME/KEY: misc.feature
LOCATION: (234220)...(234220)
DTHER INFORMATION: n equals a,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a,
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TION: (234814)..(234814)
INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LCCATION: (98239) ..(98239)
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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COCATION: (312837)...(312837)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (657081). (657081)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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OTHER INFORMATION: n equals
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LOCATION: (191995)..(19
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LOCATION: (98343)..(98
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US-08-916-421B-1/C
Sequence 1, Application US/08916421B
Sequence 1, Application US/08916421B
Sequence 1, Application US/08916421B
Sequence 1, Application US/08916421B
TITLE NEVENTION:
TITLE OF INVENTION:
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47.7%; Pred. No. 0.0042;
tive 0; Mismatches 181; Indels
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (28222)
COTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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Best Local Similarity 47.7
Matches 165; Conservative
                          US-09-902-540-1318
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661225 AAGAAAAAAAAAAAAAAAAAAAGCTAAAGAAAAAAAAGTCAAATCTGATTATACAACCTA 661166

661165 AAGAAATTAAAGAAGAGGTAAAAGCTGAAGTAGAGAAAAAAAGAAGAAGTAAAGAAAAGA 661106

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434 TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT 493

661105 TAGTACAAAAACCAAAAGCTGAAGAAGTAAAAGAAAATCAAAAACAGAAGAAAAAGAAA 661046

494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA

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660985 iagargerricricaaaraaarirrarriaaaaakerrareraargiraarigageeereeri 660926

TGCAGTAGCTGCTAAATCAGGTTTGCTTGCTCCAAGCAACTCTTATGTTGGTCAATT

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660925 crircricaacicaririricaaacricracecerrecaraaricreaaaciegageaa 660866

660865 GAATCTGA 660858 GTATCTTA 733

726

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Query Match
5.6%; Score 56.4; DB 4; Length 1664976;
Best Local Similarity 47.7%; Pred. No. 0.022;
Matches 204; Conservative 0; Mismatches 216; Indels 8;
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
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LOCATION: (741684). (741684)
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LOCATION: (779455). (779455)
NAME/KEY: misc feature
LOCATION: (779455). (779455)
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LOCATION: (1470091)..(1470091)
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1603734)..(1603734)
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314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA 373

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8; Gaps

Search completed: August 26, 2005, 07:02:59 Job time : 220 secs

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OM nucleic - nucleic search, using sw model

August 26, 2005, 00:31:21 ; Search time 4629 Seconds (without alignments) 10551.492 Million cell updates/sec Run on:

US-10-724-972A-2580 1008 Title: Perfect score:

1 ggagtggaatcagtgagagg.....gtaaaaaagataataagtaa 1008

IDENTITY NUC Gapoxt 1.0 Scoring table:

Sequence:

4708233 segs, 24227607955 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

99b htg: *
99b htg: *
99b ov: *
99b ov: *
99b pt: *
99b pt: *
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99b ro: * 5: 6: 7: 10: 11: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

							
Re	Result		Query				
	No.	Score	Match	Match Length DB	8	ID	Description
i					!		
U	-	1008	100.0	100.0 300698	-	AE016750	AE016750 Stapnyloc
ບ	7	569	56.4	110000	٦	BX571857 22	Continuation (23 o
O	ო	569	56.4	304050	٦	AP004829	AP004829 Staphyloc
υ	4	569	56.4	307750	-	AP003136	AP003136 Staphyloc
υ	L	569	56.4	347650	-	AP003364	AP003364 Staphyloc
υ	9	567.4	56.3	110000	Н	BX571856 23	Continuation (24 o
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O	80	336.2	33.4	2247	9	A64853	A64853 Sequence 10
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	10	269.2	26.7	347785	-	AP003361	AP003361 Staphyloc
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U	18	190.8	18.9	5718	9	AX951891	AX951891 Sequence
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	lus a	Continuation (12 o	Y14084 Bacillus su	TT.				AE017012 Bacillus	_	Continuation (44 o		Continuation (44 o					AR536042 Sequence	2						AF079518 Staphyloc	
	BSUB0005	CP000002_11		BSUB0006	AR537994	AE006047	AX433651	AE017012	AE017225 43	AE017334_43	AE017038	AE017355 43	BX571857_00	BX571857 01	AP004822	AR354486.	AR536042	AE017355_06	CP000001 06	AE017005	AX583941	BD237137	AR282355	AF079518	
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ALIGNMENTS

linear BCT 01-JAN-2003 section 7 of 9 of the	cus.	, Jia, J., Tu, Y.,	an Genome Center at nina		is ATCC 12228"											
DNA li 12228, sectic	12228 12228 ; Staphylocod	Fu, G., Lu, L., Lu, G.,	National Human Gai 201203, China		us epidermid				٠					RNA"	RNA"	
300698 bp ccus epidermidis ATCC enome. 8015929 G1:27316220	Staphylococcus epidermidis ATCC 12228 Staphylococcus epidermidis ATCC 12228 Batteria, Firmicutes; Bacillales; Staphylococcus	. i	Submitted (Gs. NOV-2002) Chinese National Human Genome Center Shanghai, 250 Bi Bo Road, Shanghai 201203, China	, н г	/organism="Staphylococcus epidermidis ATCC /mol_type="genomic DNA"	/strain="ATCC 12228" /db xref="ATCC:12228"	/db_xref="taxon:176280"	complement(114186) /product="tRNA-Lys"	complement (190264)	complement (269352) /product="tRNA-Tyr"	complement (369444) /product="tRNA-Val"	<pre>complement (451522) /product="tRNA-Glu"</pre>	complement (524598) /product="tRNA-Asn"	_ ^	complement (8863713) /product="238 ribosomal	complement (27182831) /locus_tag="SE1755"
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ENMSYFESKETGKKEYVFGKKGGGKKLSDELETQLFAELPLEQPTWNPNDFSPSIYQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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WLFYINIPIAIVAIILVLMTFHFPDBTQVQQSRFDIKGLIIFYIFIALLMFGLLNQHH
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GSSVGSTIMGYMYALNVGLFGSNLHNVLGLVLIIAVCLIVMMMTLYKSNTIQS"
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complement (7203. .8642)
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complement (7203. .8642)
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/transl_table=
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18584 CCTGAGCGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAA
                                      TTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCCAAAA
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Pred. No. 1.1e-77;
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Matches 728; Conserv
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Continuation 723
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IAPLAGPIF FRPINRFILIVTIITVSGILTTILCSTIYKNKLAPQGLAMSSAFNVKIGM
ILGLLGGPI FRPINRFILTLOFPRIKSEDTGGLVPCSSLLPTLAAVFLFAAIFLPLLMBYG
ILGLLGGPI FRPINRFILTLOFPRIKSEDTGGLVPCSSLLPTLAAVFLRPAIFLPELMBYG
ISTTFSVVSITFPAITANTTARQDOFFFYFYLTVVISCLIAAMIMPRINPLKNIFDEYA
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GVQNDVTAFVIGALSISQLVYLSEVGGVILGSKIPVSISKLFMIFLIRTIITLPIIAL
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ive 0; Mismatches 0;
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SSALDCSEQSVILWYETILDKIVGVIK"
                Direct Submission
Submitted (06-MAR-2002) Director-General, Biotechnology Center,
Mational Institute of Technology and Evaluation, Biotechnology
Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:blo@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
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hypothetical protein, similar to acetyltransferase
[Genomic island nu Sa 4mw]"
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hypothetical protein, similar
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[Genomic island nu Sa 4mw]"
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/gene="MW1949"
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Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
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Lancet 359 (9320), 1819-1827 (2002)
                                           CCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAA
                                                                                                                                                                                                                      ACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGAT
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APOGAS2 BA000033
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171300 GTATTAGAGTACTCATTTGCAGATGCATTAGCAGCATTAGACGTTAATCCAGTTGGTATT 171241
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PLVDEMTSNEFNIPKSWKLIAQMPFGDIREAAGEKTFNPVEDRFVIKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                      product="conserved hypothetical protein"
protein id="BAB95822.1"
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hypothetical protein, similar to SdrH"
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7808. .8434
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/transl_table=
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Best Local Similarity 73.3%;
Matches 728; Conservative (
                                                                                                                                                                                                                                                                                   7808. .8434
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FVVIFQLLNPEALKKATEQANFIYHIFIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APLITNIGYTIAKEIELEDPYENMGAKLVQEVANKTNEIAGDGTTTATVLAQAMIQEG
IKNYTSGAMPYGLRQEIDKAYKVAVERALHENSGVKERKNEIAQYGAISAADEEIGRY
ESABAKEVGUDOVITIEESNGLINTELEVVEGMQFDRGYQSPYWYDSDKWYABLERFYI
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AMFLITEAVVASIPEKKNAEPGVGFNAATNEWVNMLEAGIIVDPTKVTRSALQHAASY
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                                                                                                                                                                                                                                                                            truncated hypothetical protein, similar to integrase [Genomic island nu Sa 4mw]"
                            runcated hypothetical protein, similar to integrase (Genomic island nu Sa 4mw)"
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             note="ORFID:MW1951
                                                                                                                                                                                                                                                                    note="ORFID:MW1952
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PLCPFILDVISFAVIFINSQVGIILLFIMSCLENIILSATLKRYYEDDLKSIFYASNVIK
QGYTISKIKHAPQPRWFKQPRTABHLTSVLAEVNDEDIGAMVIKLYKLIFMLDYVLF
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ESULSFLHEKSNFRYIAFHDIELAELLKQRYENTHFNEVIENNIHFDYKIKPGKAN
TRNAIBLLKTTSPPAKIYERAKDNVSNG"
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KGLRQSLADQCKVNDIQLTIPSPRLCTDNAAMIGVAGHSLYQQGRFADLALNGHSNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein, similar to ribosomal-protein-alanine N-acetyltransfer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDQQSKEQLNIREMTKEDVPQVFDLERRSFNDSSWTIDAFYHEI
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SHTCDVMSLEVRVNNKVAQHVYENLGFQYGGKRKNYYGEGEDAMVMWVNLND"
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hypothetical protein, similar to O-sialoglycoprotein
endopeptidase"
                                                                                                                                                                                                  hypothetical protein, similar to DNA mismatch repair protein MutS"
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hypothetical protein, similar to glycoprotein
endopeptidase"
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/gene="SA1857"
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                                                                                      /gene="SA1853"
                                                                                                                                         /gene="SA1853"
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                                                                                      170940 AASTTASTCASTASGTSTSASGTGAASTTASASTTGSTAGAASTCAAAAGTGCTTCCA 170881
                                                                                                                                                                                                        170880 GCAGTAGTIGCTAAAGCTGGTTTATTAGCACATCCAAACTATTCATATGTIGGACAATTT 170821
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Mateumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Baturani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Osasawara,N., Hayashi,H. and Hiranatsu,K.
Whole genome sequencing of meticillin-resistant Staphylococcus
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Submitsed (30-JAN-2001) Director-General, Biotechnology Center, Submitted (30-JAN-2001) Director-General, Biotechnology Center, Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mall:blo@mite-go-jp, WRL:http://www.bio.nite-go-jp, GRL:http://www.bio.nite-go-jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)

On Jun 12, 2001 this sequence version replaced gi:13701842.
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                                   AAGAAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCT
                                                                                                                                                                                                                                                                   TATCTTAAAGGACCTTACTAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGGAACTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  847 AAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGAC
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/organism="Staphylococcus aureus subsp. aureus N315"
/mol_type="genomic DNA"
/strain="N315"
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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SOURCE
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155997 TTAAACGAACTAGGATTTAAAATGCATTAAGTGACGATGTAACAAAAGGTTTAAGTAAA 155938
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Pred. No. 8.6e-78;
0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="2-isopropylmalate synthase"
/protein_id="BAB43143.1"
/db_xref="GI:13701851"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ORFID:SA1862"
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/transl_table=
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Matches 728; Conser
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TLAIANEAGIDYDLERINAIAKRTPYLSKIAPSSSYSMHDVHBAGGVPAIINELMKKD
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VGGVDPSIKYTAGALTTPGRREGGARDIAHTNRAGHVVVIRYEGFKGPFGMPEMLAP
TSSIVGRGLGKDVAALTTPGRREGGARGATGAVGHISPEAAGGSPTALIEDGDEITIDLIN
RTLAVNOQPEDVLARRRESLTPPKAKVKTGYLARYTALVTSANTGGVWQVPENLI
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PENNDIDTE ISLLKBAKKPVVLAGAGINQSKSOLLTNGVRWRGI PFVTTLLGLGAVP
PSEDILFLGMGGMHGSYASNMALTECDLLINGSRFDDRLASKPDAFAPNAKI VHVUDI D
PSEINKVI HVDLGI I ADCKR PLECDLLINGSRFDDRLASKPDAFAPNAKI GEBD
VPCKPQQT IEY IGKI TINGEAL VTTDVGQHOWAAQFY PFKNHGQWYTSGGLGTMGFGI
PSSI GAKLANDDKTVVCFVDGGFQMTNQEMALLEFYGLDVKI VLINNGTLGMVKGWQ
DKFPRORFSISVFRQOPDGFQMTNQEMALLEFYGLDVKI VLINNGTLGMVKGWQ
I SPTEAVTPWVPSGKSNHEMEGL.
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AETVINAHWPOGVFYIPNCDKITPGMILAAMRTNVPAIFCSGGPMKAGLSAHGKALTL
SSMFBAVGAFKEGSISKEEFLDMEQNACPTCGSCAGMFTANSMNCLMEVLGLALPYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MRSDMIKKGDHQAPARSLLHATGALKSPTDMNKPFVAICNSYID"
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hypothetical protein, similar to acetolactate synthase
small subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ORFID:SA1859"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="ORFID:SA1858"
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trans table=
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GHSNIQIPYTITVNGTSQNILSSLITTRKNQNISYKDI ENKVKSVLYKTNRGISDIDLEL
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TSNKOLLSYKTANDAVOVKI BITVKTGTKAKADRYVPYTIANGGTSTLISKLK
ISNKOLLSYKTLNDVGYTKSKKK"
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/gene="truncated-hlb"
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3803. .4042
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locus tag="SAV1936"
57. .1443
                                                            /locus_tag="SAV1936"
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On Apr 16, 2004 this sequence version replaced gi:14247707.
This work was done in collaboration with Toshiko Ohta, Mutsumi Kanamori, Hideo Hayashi (University) of Tsukuba), Hideki Hirakawa, Satoru Kuhara (Kyushu University), Ikuo Uchiyama (Okazaki Hirakawa, Batoru Kuhara (Kyushu University), Ikuo Uchiyama (Okazaki National Research Institutes), Susumu Goto, Minoru Kanehisa (Kyoto University), Naotake Ogasawara (Nara Institute of Science and Technology) and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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                                                                                                                                                                                                                                                                                   CGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTT 966
                                   CGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M. Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A., Murakami, H., Hosoyama, A., Murakami, H., Hosoyama, A., Sakami, H., Ratico, T., Takahashi, N.K., Sawamo, T., House, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanahisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshimo, C., Kahabi, T., Hattori, M., Ogsaswara, N., Hayashi, H., and Hiramactsu, K., Mhole genome sequencing of meticillin-resistant Staphylococcus
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Hattori, M., Yamashita, A., Oshima, K. and Shiba, T.
Direct Submission
Submitted (28-FEB-2001) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@genome.ls.kitasato-u.ac.jp, Tel:81-42-778-8194,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohta,T., Hirakawa,H., Morikawa,K., Maruyama,A., Inose,Y., Yamashita,A., Oshima,K., Kuroda,M., Hattori,M., Hiramatsu,K., Kuhara,S. and Hayashi,H. Muhara,S. and Hayashi,H. Nucleotide Substitutions in Staphylococcus aureus Strains, Mu50,
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Staphylococcus aureus subsp. aureus Mu50 DNA, complete genome.
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mol type="genomic DNA"
fetrain="Mu50"
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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/db_xref="taxon:158878"
157. .1443
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AP003364 BA000017
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                                                                                                                          239356 GGAACGATGAGAGCTCTAAAACTTTTAGTATTGGGATTAATAGTTGCCTTACTTTA
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                             Length 347650;
                             Score 569; DB 1; Length 34
Pred. No. 8.3e-78;
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FRVVELDPSAKIEVTYYDKOKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVI
                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="MKIRKSILAGTLAIVLASPLVTNLDKNEAQASTSLPTSNEYQNE
KLANELKSLLDELNVNELATGSLNTYYKRTIKISGGKAMYALKSKDFKKMSEAKYQLQ
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complement (5216. .5566)
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                  AAATTAATCAATAAGTATAAAGATGAAATTAAATTTGATAGAAATCAAAAAGTGCTTCCA
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                                                                                                        GCAGTAGCTGCTAAATCAGGTTTGCTTCATCCAAGCAACTCTTATGTTGGTCAATTC
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Bacteria, Firmicutes, Bacillales, Staphylococcus
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Best Local Similarity 73.2%; Pred. No. 2e-77;
Matches 727; Conservative 0; Mismatches 266;
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 251 CATITICCAGATGCATTAGCAGCATTAGACGTTAAACCAGTTGGTATTGCTGATGGTGATGGTA 260 AAAAAAATGGTATTATAAAACCATTAAGAGAATAAATTGGAAAATACACTTCTGTAGGAA [371 CACGTAAACAGCCAAACTTAGAAGAAATTAGTAAATTAAAACCGGATTT	380 ATAATAATAGACACAAAGGTATTTATAAAAGACTTAAATAAA	440 TGAAAAGTTTCGATGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAAAAG 	500 CTTTAGGTAAAGAAGAAGAAGGTAAAAAGGCTTAGAAGAACACGATAAGAAAATTGAAG 	Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second S	620 AATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAG 	680 GTTTTAAAGAAGCATTAAGTGATGATGTTACTAAAGGTTTAAGTAAG	740 CTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAA	800 TGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTGTAT 	860 GGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACGTGACTTATGGG 	920 CAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAATTATCTA 	980 AGAAAGA 986 	1031 AAAAAGA 1037
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713 AAGGITTAAGTAAGTATCTTAAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTC 772 177 ATGITGGICAATICCIAAGICAACIAGGITITIAAAGAAGCAITAAGIGAIGAIGITACIA 712 176 AIGIIGGACAAITITIAAACGANCIAGGAITIAAAAAIGCAITAAGAGGAGGAGGAACA 117 772 61 ATTGCAACTGCAGCATGTGGAAATA---ATAGTTCAAGTAACTCAAGTAAAGAGTCATCA 117 713 ccaagirigerarrecrearcargeraagaaaaacgrarca-raacccagraaga-aa 535 353 ACTTAMACCAGATTTAMTTATTGCTGATAMTAGACACAAAGGTATTTATAMAGACTT 413 ATTAAANCCGGGATTAATTATCNCTGATAGCAGTAGACATAAGGGTATTAATAAAGAATT 416 AAATAAAATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATAT 473 TAGAAGAACACGATAAGAAATTGAAGAATATAAAAAAGAAATAAACTAATGGATAAAAATC 592 TGATGCTTTTAA-AACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCT 296 Trgcrgagcargaranantaarcaaraagraraaagargaaarraaarrrgaragaaarc CGTGTTGTTGTTCTTTGATTTCATTTG--TTGATGCGTTAGTTGC-TTTAGATGTTAAA AATTIGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAA 831 GGAGTGGGACNGATGAGAGGTCTAAAAACTTTTAGTATATTGGGATTAATAGTTGCCTTA 771 CTTTTAGTTGCAGCTTGTGGTAATACGGATAATTCAAGTAAAAGAAG-AATCATCAACTA 1 GGAGTGGAATCAGTGAGAGGTTTTAAAATTTTAAGTGTAATTGGCTTATTGTTTTTTA Gaps Indels 13; Length 2247; 814 15 ATTTAAATCCAGAGCGTATGATCATTATGACAGATCATGCTA 773 AAGTGAATCCTGAGCGTATGTTCATAATGACAAACAAAGCAA Score 336.2; DB 6; Pred. No. 6.8e-42; 0; Mismatches 229; Patent: WO 9731114-A 10 28-AUG-1997; SMITHKLINE BEECHAM PLC (GB) Location/Qualifiers . 2247
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237 652 177

532

AP003132 RESULT 9 AP003132 LOCUS

Burnham, M. K. and Hodgson, J. E. POLYNUCLEOTIDES AND AMINOACID SEQUENCES FROM STAPHYLOCOCCUS AUREUS

298050 bp

DNA

BCT 11-JAN-2003 linear

57

PAT 29-MAR-1999

linear

DNA

A64853 2247 bp Sequence 10 from Patent WO9731114.

DEFINITION

RESULT 8 A64853/c

ACCESSION VERSION

A64853 A64853.1 GI:4530844

unidentified unidentified unclassified.

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

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TVVDNGGKIYDMINDSYSKYVISDAVHIGWKGWVYMDEQIAKHMKGEPQPEVDKPKN"
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PLALVKVLQSTWLGGHQI HPHESKLI EPVGPLGI SYVTFKSVQLIMEI RDGSI KEI KV
WKLI QPI SPPPTI SSGPI DRYKR PVKDDKKVPTGNEYRELVLKAI HMIMLGFLYKYI V
                                                                                                                                                                                                                                                                   AYFINTYAIMPLOLDLHGFVNLMLYMYAYSLYLFFDFAGYSLFAIAFSYLFGIKTPPN
FDKPFKAKNIKDFMNRWHMTLSFWFRDCIYMRSLFYMSRKKLLKSQFAMSNVAFLINF
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complement(5530. .6594)
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/transT_table=
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GGSKKRMILFCHMSPYNIVGHIGAIKAGGYPVDTGS PEDBIKMIINKVOBEVPNT

TDESFELLEGEVFTIEDIKTSQDPVIFDSQIKDNDTVTIFTSGSTGEPRGVQIEYAS

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LEEIEFTGLRQSBEYVRALVENTSKNINKVIHLGAIVPTTEVTDNAEMTKNIKNDLKSR

LDEXMIPRKFEWMEQLPLTSNGKIDRKKIABVING"
                                                                                                                                                                                                                                      Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M., Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A., Mizutani-Ui, Y., Takahashi, N.K., Sawano, T., Inoue, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Sakania, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C., Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H., and Hiramatsu, K. Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-JAN-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail-1blo@mite-go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424) On Jun 12, 2001 this sequence version replaced gi:13700734.
Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
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                                                                                                                                                                                        Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                    Staphylococcus aureus subsp. aureus N315 Staphylococcus aureus subsp. aureus N315
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280_.432
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                         genome, section 4/10.
AP003132 BA000018
AP003132.2 GI:14349174
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'gene="SA0792"
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114380 CGGAGATTAGAAAGAAATTGAACAGAGTACGTTAAAATCTGCATTTGCATTCGGTATCT 114439
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
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Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
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                                                                                                                                                                                                                                                                                  GACCTTACTACAAATGAACACTGAAACTTTTATCTCAAGTGAATCCTGAGCGTATGTTCA
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                                                      114080 GCAGCACTAAAAATATAACAAAGTCAGTAAGAGATAAGATTGGGCATATGAATCGGTTG
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                                                                                                                                                                                                                                               CTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGATTG
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                                                                                                                    GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTG
                                                                                                                                                                                                                                                                                                                                                                          437 AACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAA
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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GCEDKYHNVPGAEEYTHSIOTLSKARDTFHSISELPEGAKVGIVGAGLSGIELASELR
ESSASDLEIYTYDRGPRILTRHPERLESKYVAKMPAKNNVTVVPNSNINKVPEPKIYNCD
EPKDIDLVWTAGIQPVEVVRNLPIDINSNGRVIVNQYHQVPTYRNYVVGDCADLEH
APSAQLAEVQGDQIADVLKKQMLNEPLPDRMPELKVQGIVGSLGGKQFAYIMDRTVT
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DILUVALGFVSETFGIEGMKDHAFQIENVITARELSRHIEDKFANYAASKEKDDNDLS
ILVGGAGFTGVEFLGELTDRIPELCSKYGVDQNKVKITCVEAAPKMLPMFSEELVNHA
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hypothetical protein, similar to NADH dehydrogenase"
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/codon start=1
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Pred. No. 2.9e-32;
0; Mismatches 433; Indels
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AL DNA RESEARCH 11, 51-56 (2004)

B (bases 1 to 347785)

RG Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.

Direct Submission

Life Sciences, Kitasato University; Kitasato Institute for Submitted (28-FEB-2001) Masahira Hattori, Kitasato Institute for Singences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-8555, Japan

(B-mail:hattori@genome.ls.kitasato-u.ac.jp, Tel:81-42-778-8194, Fax:81-42-778-8193)

On Apr 15, 2004 this sequence version replaced gi:14246761.

This work was done in collaboration with Toshiko Ohta, Mutsumi Kanamori, Hideo Hayashi (University) Ikuo Uchiyama (Okazaki National Research Institutes), Susumu Goto, Minoru Kanehisa (Kyoto University), Macuke Ogasawara (Nara Institute of Science and Technology) and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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VPSI QAFHVNKCRFANRCNKKLDI CNNQSPROHVCEDVI VRCHLYKNEYKEI "
                                                                                                                                                                    Ohta,T., Hirakawa,H., Morikawa,K., Maruyama,A., Inose,Y., Yamashita,A., Oshima,K., Kuroda,M., Hattori,M., Hiramatsu,K., Kuhara,S. and Hayashi,H.
Nucleotide Substitutions in Staphylococcus aureus Strains, Mu50, Mu3, and N315
Whole genome sequencing of meticillin-resistant Staphylococcus

    .347785
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Pred. No. 8.3e-31;
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KTVHKYLPLAHAYTELRKELLGLDDLKMYDLYTPLIKDI KFEMPYERAKEMHI PENVYDNIV
KTVHKYLPLAHAYTELRKELLGLDDLKMYDLYTPLIKDI KFEMPYERAKEMHIKALEP
MGEBYLANVKECLANRWYDVYENKGKRSGGYSGGAHLTNPFTLLMWSNTISDLYTLVH
EPGHSAHSYFSKKOPSNSSDYITFVARVASTCNBALLSDYMDKHLDDERKLLLLNOG
LERFRATLFROTMFABEEHKIHAI EERGEPLTPTRMMESYALLNYGFTLLNOG
SKEWSRIPHFYMNYYYYQYATGYSAAQSLSHQILTECKPAVDRYINEFLKKGSSNYPI
EILKNAGVDMTTPEPIEQACEVFEQKLNAFEKLMKA"
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HYRDLEKQUSQUMPQQIQYLGGHKYVSRCNAKIIELFNBAPCDYHAVYKLSKPAINQY

HYKCRWQNSVLEPTLSAMYQLQLTDQRYVYNYGYIFPEQIYIENHPIEWQLQYDLMKK

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llarity 55.4%; Pred. No. 2.8e-32;
Conservative 0; Mismatches 433;
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                  antigens
                                                                                                                                                                                                                                                                                                                                                                                                              141 AAATCCTAAACGTGTTGTTGTATTAGAATATAGTTTTTGCTGATTATTTAGCAGCATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAAATCGTATTATTAAAACCATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACATTTATGGGACAATTCTTAATTAAAATGGGTATTCAACCTGAAGTCACAAAAGACAA
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                                                                                                                                                                                                                                                        48 ATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAA
                                                                                                                                                                                                                                                                                      <u> aciagiticirciteatectaatittacttetaceactagecegeitictegicaaaagatac</u>
                                                                                                                                                                                                                                                                                                                       AGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAA
                                                                                                                                                                                                                                                                                                                                                     TGAAGAGAAAACTGAAATGACGACAATAAAAGATGAATTAGGAACTGAAAAATTAAGAA
                                                                                                                                                                                                                                                                                                                                                                                      ACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGAAACCTGTTGGTATTGCAGATGATGGTAGCTACTAAAAATATAACAAAGTCAGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u> AGATAAGATTGGGGCATATGAATCGGTTGGATCTAGACCGCAACCGAATATGGAAGTGAT</u>
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Minh, D.B., Vytvytska, O., Etz, H., Dryla, A., Weichhart, T., Hafner, M.,
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Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail-bio@nite.go.jp, URL:htp://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Pass:81-3-3481-8424)
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Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,
Yamamoto,K. and Hiramatsu,K.
Genome and virulence determinants of high virulence
community-acquired MRSA
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Continuation [11 of 28] of BX571857 from base 1000001 (BX571857 Staphylococcus aureus
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      CAAAGTTTATGACGTTGACCGAAATAAGTGGTTGAAATCAAGGGGGATTATCGCAAGTGA
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Pred. No. 3.6e-31;
0; Mismatches 437;
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PRFTKAGVPPHFVMLPBATYAPPIPITAFGPALLTKVGVYATARTLSHESDNVSBSH
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LHDMLVKLALFLLIGIMIKITGTADIRQFGGLIKRYPVIGWSFFIAALSLAGIPPLSG
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VSEGFGLLQAVGKGSKHKPRLVTITYMGKDKDRAPIALVGKGITYDSGGYSIKTKNGM
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MMYUGLIYTLGIGSSFATIPIIASLFIPFGASIGLDTWALIALIGTASALGDSGSPA
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VEWTYDFRGERLVLADAVYTANQYGBSVIMDFNTTGAAIVALGDDKAAAFESNSKVI
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/transl_table=11
                                   . .290150
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mol_type="genomic DNA"
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                                                                                                                                                                                            db_xref="taxon:196620"
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   Location/Qualifiers
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/gene="ampA"
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EX571856_28 2800001 2902619
Continuation [11 of 29) of BX571856 from base 1000001 (BX571856 Staphylococcus aureus
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54194 AATTGTTTGGAGGTAAATGTGTGAATAGGAATATCGTTAAATTAGTTGTGTTTATGCTAA 54253
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Best Local Similarity 54.3'
Matches 539; Conservative
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Fragment Name BX571856_00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
/producE=1ma+/H+ antiporter subunit"
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/db_xref="GI:21204000"
/translation="manRQONDLILQFAAVIIFFMVMVFGFSLFLAGHYTPGGGFVGGL
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YLTTIAIVAVVITVLYGLSADYLYPMVKAGAETFYNPSTYVKAVLGGK"
complement (9275. .9616)
                                                                                                                                                                                                                                                                                                                                                             /trānslation="MEIIMIFVSGILTAISVYLVLSKSLIRIVMGTTLLTHAANLFLI
TMGGLKHGTVPIYEANVKSYVDPIPQALILTAIVIAFATTAFFLVLAFRTYKELGTDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 ACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCGATTCCTAAGTCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGITTPAAATTTTAAGTGTAATTGGCTTATTGTTTTTTAATTGCAACTGCAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 GTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCA
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                                                                                                                                                                                                                                                                      product="Na+/H+ antiporter subunit"
protein_id="BAB94697.1"
db_xref="G1:21203999"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.1%; Score 262.8; DB 1; Best Local Similarity 55.0%; Pred. No. 2.8e-31; Matches 541; Conservative 0; Mismatches 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (9616. .10044)
/gene="mnhB"
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                                                                                                                              complement (9275. .9616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="ORFID:MW0833"
                                                                                                                                                                                    note="ORFID:MW0832"
                                                                                                                                                                                                                      codon start=1
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                            1 TITATIAGCACATCCAAACTATTCATATGTTGGACAATTTTTAAACGAACTAGGATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACAATTAGACACTGAACATTTAGCTGATTTAAATCCAGAGCGTATGATCATTATGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             867 ATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GIIGAAIGCAGIIAAAAATAAICGCGIGGAIAIIGIIGIIGIIGIIGIIGIIGGGCAAGAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 TITGCTTGCTCAACCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                      TITGCTTGCTCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA
             Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. Rosen, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.1%; Score 222.6; DB 6; Length 668; 74.8%; Pred. No. 1.7e-24;
                                                                                                                                                                                                                                Length 668;
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                                                         Staphylococcus aureus polynucleotides and sequences Patent: US 6593114-A 355 15-JUL-2003; Location/Qualifiers
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larity 74.8%; Pred. No. 1.7e-24;
Conservative 0; Mismatches 94;
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                                                                                                                                             /organism="unknown"
/wol_type="genomic DNA"
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(bases 1 to 668)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54734 AAATATTAGCGGAQATTAGAAAAAAATTGAACAGAGTACGTTAAAATCTGCATTTGCAT 54793
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  54254 TCTTAGTTGTAGCAGTAGCGGGTTGTGGTCAAAAGATACTGAAGAGAAAAACTGAAATGA 54313
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                                                                                                                                                                                                               CGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                788 GIAIGIICAIAAIGACAAACAAAGCAAGIICIAACGAACCIICACIAAAAGAACIAGAAA
                                         TIGAAAICAAGCACGAAGAAGGIACIACGAAAGIACCIAAACACCCIAAAACGIGIIGIIG
                                                                                 54314 CGACGATAAAAGATGAATTAGGAACTGAAAAATTAAGAAAATCCGAAACGTATTGTTG
                                                                                                                             TTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAG
                                                                                                                                                                                                                                                       54434 CAGATGATGGTACTAAAAATATAACAAAGTCAGTAAGAGATAAGAGATTGGGGCATATG
                                                                                                                                                                                                                                                                                                CTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATT
                                                                                                                                                                                                                                                                                                                           368 TAATTATTGCTGATAATAGACACAAAGGTATTTATAAAAGACTTAAAATAAAATTGCTC
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Homologous recombination into bacterium for the polynucleotide libraries
Patent: Wo 3095658-A 20 20-NOV-2003;
Novozymes A/S (DK)
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0; Mismatches 357;
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Sequence 20 from Patent W003095658.
AX951891.1 GI:40782280
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Best Local Similarity 55.0%;
Matches 488; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          987 TAGTAAAAAGAT 999
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ACCESSION
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TITLE
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complement (7582. 7596)
complement (7600. 7737)
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           source
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Kunst, F., Ogasawara, Moszer I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Brans, M., Brignell, S.C., Bronillet, S., Bruschi, C. V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Pujite, M., Pujite, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Garadi, G., Guy, B.J., Haga, K., Haich, J., Harwood, C.R., Henaut, A., Hilbert, H. Holasppel, S., Hosono, S., Hullo, M.F., Kraein, C., Kobayashi, Y., Kochter, P., Karlenda, M., Karlen, C., Medina, D., Kasahara, Y., Karlenda, M., Karlen, C., Medina, N., Levine, A., Liu, H., Masuda, S., Mauel, C., Medina, N., Menoe, D., O'Reilly, M., Ogawa, K., Ogawara, A., Oudega, B., Perscott, A.M., Parro, V., Pohl, T.M., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Sachie, F., Sato, T., Rivolta, C., Rocha, E., Roche, B., Rese, M., Sadaie, Y., Sato, T., Sekiguchi, J., Schleich, S., Schroeter, R., Soldo, B., Schwekka, A., Seoro, S.J., Serror, P., Shin, B.S., Soldo, B., Scrotian, R., Tarakoshi, A., Tarakoshi, A., Tarakoshi, A., Tarakoshi, A., Tarakoshi, A., Tarakoshi, A., Tarakoshi, A., Wambutt, R., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamamoto, H., Wambutt, R., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamamoto, H., Wamane, K., Yoshikawa, H.F., Zumstein, R., Yoshikawa, H.F., Zumstein, R., Yoshikawa, H.F., Zumstein, R., Yoshikawa, H.F., Zumstein, R., Yoshikawa, H.F., Zumstein, R., Yoshikawa, H.F., Zumstein, R., Yashikawa, H.F., Zumstein, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (Dases 1 to 197409)
                                                                                                                                                                                                                                                                                                                                                                                                                                 26011 GCCAAAGATGTGCTTAAAAAGTGTATAATAAATAGGACAAATGAGAA 26058
                                                                                                                                                                                                                                                                                                                                                                       25840 ATCGATCTGATATTTTGTTCATCTCAGCCAACGAAGGCAAAACCATTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BSUB0005 197409 bp
Bacillus subtilis complete genome
1011078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 197409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z99108 AL009126
Z99108.2 GI:32468715
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Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98044033
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BSUB0005/c
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAATCGCCCCGACGATTGAATTAAAAGCCGTGAAGCGACATATGACGAAACGATC 25569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAGCTTTACGACCATTGCTAAAGCATTAAATAAAGAAGATGAAGGAAAAGAAAAGCTT 25629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGAGCACAAAAAGTCATCAACGATCTAAAAGCCGAACTTCCGAAAGATGAAAACCGC 25689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACATCGTTCTCGGCGTTGCAAGAGCGGATTCCTTCCAGCTTCATAATACATCATCCTAT 25749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25272
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /procedin id="BAA22300.1"
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AGTWHTGFPIMMFGLPAACLAMVVTARPSKRKATAGWHIGALTATITITESTIEFA
FWFLSPLLYANHAVITGLSLEFVNWLGIRSGFSFSAGAIDYVLSYGIAEKPLILLLUS
TCYAAVYFIVFYVLIKALNKTPGRREDDDVDEVLDGNTVQDVNENIMLKGLGGKENLQ
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                                                                                                                                                                                             TIDHCATRLRLTVKDTALVDEALLKKAGAKGVVKSGGQSVQVIIGPNVEFAAEELRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGTTGGGATAGCGGATGATAACAAAAAAAATCGTATTATTAAACCATTAAGAGATAAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 AATAAAATTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25213 TCTAAGGATTCCAGAGTGATCCATGACGAAGAAGGAAAAACGACAGTAAGCGGCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccerrecerreceacarcaacaacaaaaaaaaarcarraaaaaacrrerececaecrec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 190.8; DB 1;
Pred. No. 4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTFKTPDKSMVAQVEHTIVITKDEPIILTKL"
12166. .12183
12181. .12495
                                                                                                                                                                                                                                                             complement(11176. .11195)
                                                                                                                                                                                                                                                                                                                                                /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12181. .12495
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                                                                                                                                                                                                                                                                                             11334. .11352
11350. .12099
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55.0%;
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Best Local Similarity
Matches 488; Conserv
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/ LTERELATION="MSKGYYSILFSQTTTNIGFSLYTMVVISFLFKMTNSTTIASMVT
LISIIFRIFGSAILPLITTRLKLPLTIISQLIQMLLLICIEFYALLRTYSNOTLILVF
LISCISFPRGWFSPLKSPLKSTIGEIISPDRVVKARDLSTVDQTPQFYGWSLGGLIAF
LGEGYTILLTIFLLFLTSLLSLLFCLPHGHANSVIRENGSPKKSIVSGWRXLFSQKKLR
TIIIMDLIESWAGMIWIGSV9LAFVNEVLHKGESWWGFINGAYYLGSMIGGFIIYKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKHEELVMLKNY POQNGI LPNNFDFEEKI PQSI.IEEFEKTEEDGMÎLI PGGFFEFGLN
BENEI DPKTFWKDAVPRQWALDPFET DKY PVTNKOVOI FFEFI EBGUHI FCHPNEPQ
RKOHRRNITWHDRY LDNHPVTGI DFY DAFAYAR KGKELPTEFQWEKAARGEKANVWP
WQDKFDPAKVQYAGSLYNEPI TSLKGWRENLLKAHADKELNHLTSDI FEQNGESPYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERFONKLINFMLIGAVSYGSLTLIYGFISNSYLALILVLFMGPAYLLADLTOGETLION
ITTEOTRIN MSARGSLVQFIFMFSILAIGAISDFLGVRLVYVSAGILLLVSAIYGFS
QLOFKKKVNKHISF"
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DLVSPKAMDVCANHKIEESVAYLSSIIDDVRESISYPKKPVGLGAQKVLSTLLDIFGV
                                                                                                                                                                                                                                                                                                                                                                                                                          YFDNVGGPISDAVMNLLNEFARIPVCGAISSYNAESEADDMGPRVQSKLIKTKSLMQG
PIVSDYSDRFSEGAKQLAEWLKAGKLHYBETITEGFENIPDAFLGLFKGENKGKQLIK
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/db_xref="UniProt/TrEMBL:034440"
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/note="similar to quinone oxidoreductase"
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/db_xref="UniProt/TrEMBL:034890"

/translation="MRKLRKNWRKSIVSPVLYTNEKW"
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complement(4979. .6199)
                              complement (3478. .4497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4979. .6199)
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function="unknown"
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5535. .7998
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gene="yfmg"
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ARNKARVSTRUMAMSRQKKLDKMDH ELAAEKPREPHFKPRATSGKLI FETKOLVIG
YDS PLSR PLALRAMERGQKIL AYGANGIGKTTLLKSLLGE I QPLEGSVERGEH I YTGYF
RQEVKETINNYTCI EEGWSR PFS YTQYE I RAAPAKCGLTYKHI ESRVSVLSGGEKAKVF
LCKL INSETNILVLDEPTNHL DADAKEELKRALKEYKGS I LLI SHEPDFYMDI ATETW
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EIYNKMGEADPDELEKLLEEVGVIQDALTNNDFYVIDSKVEEIARGLGLSDIGLERDV
TDLSGGQRTKVLLAKLLLEKPEILLLDEPTNYLDEQHIEWLKRYLQEYENAFILISHD
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KMERAKIIATPEDGEFPLLLATDIAARGLDIENLPYVIHADIPDEDGYVHRSGRTGRA
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This entry contains data from release R16.1 of the Subtilist database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/Subtilist/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSILSVKDLSHGFGDRAIFNNVSFRLLKGEHVGLIGANGEGKST
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complement (52. .1608)
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2979. .3425
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               Length 197409
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                                  Indels
                                   0; Mismatches 357;
               DB 1;
             Score 190.8; DB 1
Pred. No. 2.6e-20;
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             18.9%;
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             Query Match
Best Local Similarity 55.04
Matches 488; Conservative
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11459 TCGATGAAGACGGGAAAAGACCGATCGAAAAAGATCCTCTTTGGAAAAAGCTCAGCGCAG 11518
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van Sinderen,D., ten Berge,A., Hayema,B.J., Hamoen,L. and Venema,G.
Molecular cloning and sequence of comK, a gene required for genetic
competence in Bacillus subtilis
Mol. Microbiol. 11 (4), 695-703 (1994)
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Park,S.S., Wong,S.L., Wang,L.F. and Doi,R.H.

Bacillus subtilis subtilisin gene (aprE) is expressed from a sigma
A sigma 43) promoter in vitro and in vivo
J. Bacteriol. 171 (5), 2657-2665 (1989)
89213955
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                                                                                                                                        878 TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA 937
                                                                                                                                                                                                                    comk gene; yhfO gene; yhfP gene; yhfQ gene; yhfR gene; yhfV gene;
yhfT gene; yhfU gene; yhfV gene; yhfW gene; yhxC gene; yhxD gene.
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Bacillus subtilis chromosomal DNA, region 78-80 degrees: aprE to
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1 (bases 1 to 104)
Stahl,M.L. and Ferrari,E.
Replacement of the Bacillus subtilis subtilisin structural gene with an In vitro-derived deletion mutation
3. Bacteriol. 158 (2), 411-418 (1984)
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                                                           818 CTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTG
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Noback, M.A., Terpstra, P., Holsappel, S., Venema, G. and Bron, S.
Direct Submission
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/organism="Bacillus subtilis"
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/strain="168"
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QGAVDPVGGKQLASILSKIQYGGSVAVSGLTGGGEVPATVYPFILRGVSLLGIDSVYC
PMDVRAAVWERMSSDLKPDQLLTIVDREVSLEETPGALKOILQRKVIWKL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.coli (Swiss Prot P36942), and to several phosphoglycerate mutase (pgm) proteins, from Treponema pallidum (EMBL: U55214) and Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="high similarity to yhdH from E.coli (Swiss Prot
P26646), and lower to many alcohol dehydrogenases."
12. From 101. 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="UniProt/TrEMBL:007614"
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                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
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/db_xref="GI:2226251"
                                                                                                                                                               cerevisiae (Swiss Prot P39979),
/citation=[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GOA:007614"
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2043. .2056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /producTe="hypothetical protein"
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complement (3722. .3731)
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iadgaaallvmebekaaalgikpvirpissavsgihdnfppaapvvairqlinvt
pddidlfeineafavkicvcsqelgipfskinvrggalalghpygasgaalvtrlfye
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I FVKSPMRFSGYVNGSTPDEWMTVDDMGYVDEEGFLYISGRENGMIVYGGLNIFPEEI
ERVLLACPEVESAAVVGIPDEYWGEIAVAVILGNANARTLKAMCKQKLASYKIPKKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similarity to long-chain-acyl-CoA synthetase from B.subtilis (EMBL: 275208), bile acid-CoA ligase from Eubacterium sp. (Swiss Prot P19409), long-chain-fatty aciduCoA ligase from E.coli (LcfA; Swiss Prot P29212)."
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/gene="yhfu"
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Prot P22819)."
                                                                                                                                                                                                                              complement (3788. .4882)
                                                                                                                                                                                                                                                                                                  complement (3788. .4882)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reraraccaceregarcerereredererecececececateracacegedeaarec 3058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2702 cgrgcirringarcegaaaracaaarcaraccarrareeccaegegargaaaacrrcrrrac 2761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2762 ATCGAGACTTT---TAACACGTCGGCTACCGATATGCAATCAGTACGTCAGGCAATAG
                                                                                                                                                                                                                                                                             AGAACATAAAGTGGCGGTAACACATGATTTAGGGAAGACAAATGTGCCTGAGCATCCGAA
                                                                                                                                                                                                                                                                                                                                                                                            2282 GCGGGTTGTTGTTCTTGAGCTAGGTTTTATTGATACACTGCTTGATCTCGGCATTACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAAACTTAGAAGAAATCAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2462 ATTAAAACCCGATTTAATTGCTGACACGACCCGGCATAAGAAGGTGTACGATCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2522 GAAAAAAATAGGGGGGGAGGATTGCACTTAATAATTAAATGCTGATTATCAGGATACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 AGAAGAACACGATAAGAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 TGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 AGTGAATCCTGAGCGTATGTTCATAATGACAAAGCAAGGTTCTAAGGAACCTTCACT
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                                                                                                                                                                                                                           117 AAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAAGAACACCCTAA
                                                                                                                                                                                                                                                                                                                                     177 ACGIGITGITGITCITGAGIATTCATITGITGATGCGTTAGITGCTTTAGATGTTAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGGGATAGCGGATGATAACAAA---AAAAATCGTATTATTAAAACCATTAAGAGATAA
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                                                                                                            Length 12556;
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                                                                                                                                                                    Indels
                                                                                                               DB 1;
                                                                                                                                      Pred. No. 2.5e-16;
                                                                                                            16.5%; Score 166.6;
llarity 51.5%; Pred. No. 2.5.
Conservative 0; Mismatches
                       /gene="yhfT"
complement(6329. .6336)
complement (6329. .6336)
                                                                                                                                            Similarity
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Matches 46
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                                                                                                                                                                                    Bacillus subcilis subceps subcillas str. 168

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 198743)

Stavedo, V. Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Berneri, E., Capasawara, N., Brass, A., Braun, M., Brignell, S.C., Borriss, R., Bunschi, C.V., Caddwell, B., Caphano, V., Carter, N. M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emerson, P.T., Entian, K.D., Errington, J., Fabrer, C., Errari, E., Foulger, D., Fritz, C., Guy, B.J., Haga, K., Haich, S.D., Galizzi, A., Galleron, N. Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, B.J., Grandi, G. Guiseppi, G., Guy, B.J., Haga, K., Haich, J., Harwood, C.R., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Khaert-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Kauber, J., Laarevoic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medine, N., Melindo, R.K., Lapidus, A., Liu, H., Masuda, S., Mauel, C., Medine, N., Mone, D., O'Reilly, M., Ogawa, K., Odiwara, A., Oudega, B., Park, S.H., Parco, V., Pohl, T.M., Porteelle, D., Porwollik, S., Prescott, A.M., Prescean, B., Park, S.H., Parco, V., Sako, T., Schleich, S., Schroeter, R., Scoffone, F., Sako, T., Takeuchi, M., Tamakoshi, A., Tanaka, T., Takabashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Tarpstra, P., Tognoni, A., Tanaka, M., Waller, E., Waller, H., Waitzenegger, T., Winters, P., Wanbutt, R., Wanbutt, R., Wanbutt, R., Wanbutt, R., Wanbutt, R., Wanbuct, R., Wanbanoto, K., Yasumoto, K., Yasumoto, K., Yasumoto, K., Yasumoto, K., Yasumoto, K., Yasumoto, M., Wander, P., Wanganoto, H., Yasumoto, K., Yasumoto, K., Yasumoto, A., Wanganoto, H., Wanne, R., Yasumoto, M., Wanne, R., Yasumoto, M., Wanne, R., Yasumoto, M., Wanne, R., Yasumoto, M., Wanne, R., Yasumoto, M., Wanne, R., Yasumoto, M., Wanne, R., Yasumoto, M., Wanne, M., Yasumoto, M., Wanne, M., Wanne, M., Wanne, M., Wanne, M., Wanne, M., Wanne, M., Wanne, M., Wa
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On Jul 7, 2003 this sequence version replaced gi:2633260.
This entry contains data from release R16.1 of the Subtilist database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.ff/Subtilist/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Submission

Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur,

Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724

Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,

adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transT_table=11
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7]
7[unctIon="cell wall lytic activity"
7]
7] note="alternate gene name: cwlE, yhdD"
                                                                                                                                       Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
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/strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:224308"
complement(38..1504)
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complement(38. .1504)
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/transl table=
to 1209781.
299109 AL009126
299109.2 GI:32468723
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                                 ACCESSION
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KEYWORDS
SOURCE
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TITLE

COMMENT

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/db_xref="Uniprov150"
/db_xref="Uniprov150"
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GIYLGNGETIANDSGVVISNNNNSYWKQRYLGAKRYF"
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LAFGLSFGLGGKDFASRYLSTFERKMQNTEIEKNRKNQNPPNDM"
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HIDPSLVRPKLQMSVDDEBEEEIEGAATPYDDLMSLDEKKPKKQVKKSKKPFPPRPEKD
ILLFIEEHSRELEPWQRDILTMMREEMLYFWPQLETKIMNEGWASYWHQRIIRBLDLT
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LLGWAAASVLSFLVKKIGMKLNTSDKLRKWNLVSEGKDIHQAVNTASQIVFYLVLLVF
LPGVLSSLKISGISGPFTNMMESVLAFLPKLFAAALIVLIGWLVARLVRDIITNFLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKLTNYTDYSLRVIFLAAERPGELSNIKQIAETYSISKNHLMK
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complement (2200. .3858)
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/function="involved in spore cortex synthesis (stage V
muropeptidase (major autolysin) (CWBP49')"
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/db_xref="UniProt/Swiss-Prot:007573"
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complement(1657. .2097)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (1657. .2097)
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3889. 5295
/gene="spoVR"
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function="unknown"
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function="unknown"
                                                                                              xref="GOA:007532"
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/codon start=1
/trans1_table=1:
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96568 CGTGCTTTTGATCGGAAATACAAATGATACCATTATGGCCAGGGATGAAAACTTCTTTAC
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                                        96388 GAAAAAATAGCGCCGACGATTGCACTTAATAATTAATGCTGATTATCAGGATACAAT
                                                                                                                                                                                                                                         TGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAAACGCTT
                                                                                                                                                                                                                                                                                                 96448 TGACGCTTCGCTTACGATTGCAAAAGCAGTCGGCAAGGAGAAAGGAAATGGAGAAAAAGCT
                                                                                                                                                                                                                                                                                                                                                         AGAAGAACACGATAAGAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCA
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                                                                                                                         AAATAAAATTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATAT
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Pred. No. 3.2e-15;
); Mismatches 50
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Staphylococcus aureus polynucleotides staphylococcus aureus patent: US 6593114-A 2556 15-JUL-2003;
Location/Qualifiers
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6593114.

    .242
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    /mol_type="genomic DNA"

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Sequence 2556 from patent US
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AR356438.1 GI:33762522
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PRYLGAKRF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96148 GCGGGTTGTTCTTGAGCTAGGTTTTATTGATACACTGCTTGATCTCGGCATTACGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus tag="BSU09420"
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                                                                                                                      complement (5325. .6710)
                                                                                                                                                                                                                   complement (5325. .6710)
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                                                                                                                                                                                    Tocus tag="BSU09410"
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complement (3197. .3739)
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               Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                               Zhang, Q. and Kapur, V.
Direct Submission
Submitted (24-OCT-2000) Department of Veterinary Pathobiology
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
                                                                        and
                                                                                                                                                                                                                                                                                               1. .13792
/organism="Pasteurella multocida subsp. multocida
pm70"
             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurell
Pasteurellaceae; Pasteurella.
1 (bases 1 to 13792)
May,B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S.
                                                                                  Complete genomic sequence of Pasteurella multocida, Pm
Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
21145866
Pasteurella multocida subsp. multocida str. Pm70
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   ORGANISM
                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
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                                                      REFERENCE
AUTHORS
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MEDLINE
PUBMED
                                                                                                                                                                                        REFERENCE
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                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                PAT 08-OCT-2004
                                                                                                                                                                      447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                          121
                                                                                                                                     181
                         CGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAAG 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 242)
Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 AGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCCAAACTTAGAAATTAGTAAATTAAAACCGGATTTAATTATCGCTGATAGCAGT
                                              62 CGTATCATTAAACCAGTTAGAGAAAAATTGGGGATTATACTTCTGTAGGTAACGTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus polynucleotides and sequences Patent: US 6737248-A 2556 18-MAY-2004; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 79.3%; Pred. No. 3.2e-15; 91; Conservative 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2556 from patent US 6737248.
AR537994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
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Matches 191;
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Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candelon, B.,
Kaparral, V., Bhattacharyya, A., Reznik, G., Mikhailova, N.,
Lapidus, A., Chu, L., Mazur, M., Goltsman, E., Larsen, N., D'Souza, M.,
Walunas, T., Grechkin, Y., Pusch, G., Haselkorn, R., Fonstein, M.,
Ehrlich, D.S. D., Overbeek, R. and Kyrpides, N.
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                                                                                                                            raaagccccarrraarrarreccarrccagccagccacacccccrrargaraagcrgr
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                TTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAAACTTAGAAGAAATCAGTAAAC
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Methods for monitoring multiple gene expression
Patent: WO 0229113-A 2066 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S (DR
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Pred. No. 2.1e-13;
0; Mismatches 376;
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Sequence 2066 from Patent W00229113.
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Bacillus licheniformis
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ILTMAGYLEARPRVGYFYTGKTGGQLLSEAVKKIKVQDYQSRPVVIDKNVSVDAICT
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ATYANINRIQBEIDHPBEVISRINCQVIDVSNKAIEETANIIVNAVQNQKMF"
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The number of ribosomal RNA operons in Bacillus cereus
Unpublished
3 (Dases 1 to 30132)
8 Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candelon, B.,
Kapetral, V., Bhattecharyya, A., Reznik, G., Mikhailova, N.,
Lapidus, A., Chu, L., Mazur, M., Golleman, E., Larsen, N., D'Souza, M.,
Walunas, T., Grechkin, Y., Pusch, G., Haselkorn, R., Fonstein, M.,
Ehrlich, D.S.D., Overbeek, R. and Kyrpides, N.
Direct Submission
L. Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de
Vilvert, Jouy en Josas 78352, France
Location/Qualifiers
I. 301332
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//db_xref="ATCC:14579"
//db_xref="ATCC:14579"
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IAFSGRALGDDTPKYLNSPETPIFHKSKLLYNFHQARPFIRKRGQVVLFEGTADVLAA
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PADQAAKVADWLSKKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           producE="Membrane-attached cytochrome c550"
protein id="AAP11201.1"
db_xref="GI:29897927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (2044. .3840)
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complement (114. .470)
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complement (857. .1984)
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          AUTHORS
TITLE
JOURNAL
REPERENCE
AUTHORS
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of AE017225 from base 4300001 (AE017225 Bacillus anthracis str.
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                                                                                                                                LOCUS AE017225 Accession AE017225
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Pred. No. 5.2
                                 241057 GCTGATGCAAAAGCAAAAT 241076
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   GAAGAATATAAAAAAGAAAT
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                                                                                                                                                   Fragment Name
AE017225_00
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AE017225_19
AE017225_20
AE017225_21
AE017225_22
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AE017225_15
AE017225_16
AE017225_17
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Continuation [44
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AE017225 09
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AE017225_31
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Best Local S:
Matches 308
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WPCOMMENT
                                                                                                                                     Sequence
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Pred. No. 1.3e-13;
0; Mismatches 241;
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complement(8281. .8679)
/locus_tag="BC4298"
/EC_number="3.5.4.5"
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/transl_table=11
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'transl table=
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Conservative
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Matches 310; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The genome sequence of Bacillus anthracis Ames and comparison to
Bacillus anthracis str. Ames section 15 of 18 of the complete
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Nature 423 (6935), 81-86 (2003)
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similarity; putative"
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AE017038.1 GI:30259002
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COMPLEMENT (3820. .4431)
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EDSLHGNKAEVRNVTDKNGNILETINVSKGQSGNNLNLTIDMELQKRVEEIITKNLLR
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complement (2427. .3704)
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243602 CAACAACCAAACTTAGAAGAAATTAGCCGTTTAAAACCAGATTTAATTATACACGCTTCA 243661
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                                            243542 AATAAATGGGTAAATACAAAACAAAACCGAGTAAAGATGTTGTAGATGTCGGGACACGT
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GB:M60520, GB:M60521, GB:X59065, GB:X65778,
SP:P05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATTTTAAGTGTAATTGGCTTATTGTTTTGTTTTAATTGCAACTGCAGCATGTGGAAAT
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.
                                                             product "conserved hypothetical protein"
protein id="AAP28211.1"
db_xref="GI:30259006"
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protein id="AAP28212.1"
db_xref="GI:30259007"
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Pred. No. 4.1e-13;
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complement (7513. 7926)
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5329. 7432
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/gene="gcpE"
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Staphylococcus aureus subsp. aureus MSSA476
Staphylococcus aureus subsp. aureus MSSA476
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
Barton,A., Bason,N., Bentley,S.D., Chillingworth,C., Cronin,A., Chillingworth,C., Curncher,C., Clark,L., Corton,C., Cronin,A., Doggett,J., Churcher,C., Clark,L., Corton,C., Cronin,A., Holroyd,S., Jagels,K., James,K.D., Lennard,N., Line,A., Mayes,R., Moule,S., Mungall,K., Ormond,D., Quali,M.A., Rabbinowitsch,B., Rutherford, K., Sanders,M., Sharp,S., Simmonds,M., Stevens,K., Whitehead,S., Barrell,B.G., Spratt,B.G. and Parkhill,J.
Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance in Proc. Natl. Acad. Sci. U.S.A. 101 (26), 9786-9791 (2004)
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GKTHLMHAIGHHVLDNNPDAKVIYTSSEKFTNEFIKSIRDNEGEAFRERYRNIDVLLI
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DITPPDYETRMAILQKKIEBEKLDIPPEALNYIANQIQSNIRELEGALTRLLAYSQLL
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QIAMYLSRELTDFSLPKIGEEFGGRDHTTVIHAHEKISKOLKEDPIFKQEVENLEKEI
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protein_id="CAG41773.1"
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Submitted (23-JUN-2004) Submitted on behalf of the Pathogen
Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, E-mail: mh3@sanger.ac.uk
Location/Qualifiers
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BK571857 2799802 bp DNA circular BC
Staphylococcus aureus strain MSSA476, complete genome.
BK571857
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BX571857_15
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BX571857_2
BX571857_2
                                                                                                                          BX571857
                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAAT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGTACTACGAAAGTACCTAAAACACCCTAAAACGTGTTGTTGTTCTTGAGTATTCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26613 CAACAACCAAACTIAGAAGAAAITAGCCGTITAAAACCAGATTTAATTATCACAGCTTCA
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                                                                                                                                                                                                                                                                                                                            AAAATTTTAAGTGTAATTGGCTTATTGTTTGTTTAATTGCAACTGCAGCATGTGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                      85 AATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                         26373 GAGGAGAAAAAAGAAACAAAAGCGGACAATAAAAATCAAGCTATAACAATTAAACGCT
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                                                                                                                                                                                                                                                 Length 110000;
                                                                                                                                                                                                                                                 Score 140; DB 1; Length 11
Pred. No. 1.6e-12;
0; Mismatches 245; Indels
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                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.6%;
Matches 306; Conservative
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AE017355_43
AE017355_43
AE017355_44
AE017355_45
AE017355_46
AE017355_47
AE017355_48
AE017355_50
AE017355_50
AE017355_51
AE017355_51
AE017355_51
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BX571857 00/c
WPCOMMENT
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103882 TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC------AACAG 103836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104122 GGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 104063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104002 ACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAAGAACC 103943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103942 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT 103883
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="DNA gyrase subunit B"
/product="DNA gyrase subunit B"
/protein_id="CAG4177.1"
/db_xref="G1:49243360"
/translation="WTALSDVNNTDNYGAGQIQVLEGLEAVRKRPGMYIGSTSERGLH
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TVLHAGGKFGGGGYKVSGGLHGVGSSVVNALSQDLEVYVHRNETIYHQAYKKGVPQFD
LKEVGTTDKTGTVIRRKADGBIFTETTVYNYETLORINEFALNKGIGTLRDRENDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENVREDS YHYEGGIKSYVELLARBKEPIHDEPIYİHQSKDDIEVELAIQYNSGYATNI
ITTAANI HYEGGHHEDGYRKALITRINIS YGLSSKIMKEBERDELSGEDFEGWATIS
IKHGDPQFEQCOKTKLAGNSEVRQVUDKIRSEHERELYENPOVARTYVEKGIMAARAR
VAAKKAREVTRRKSALDVASLPGKLADCSSKSPEECEIFLVEDPOVARTYVEKGINAARAR
VAAKKAREVTRKKSALDVASLPGKLADCSSKSPEECEIFLVEDBSAGGSTKGGRBSRT
ONDGAHIRTLILIYEYREMELIS TROMITARFGTGGGBDEDLAKARKIVINTDA
DVDGAHIRTLILILIYEYREMELISAGYYYIAQPPLYKLTOGKÇKYYYNDRELDKLKS
ELNPTPKWSIARYKGIGEMNADQLMETTMNPEHRALLQVKLEDAIEBADÇTFEMLMGDV
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                                                                                                                                                                                                                                                                                                                                                                               'note="Ortholog of S. aureus MRSA252 (BX571856) SAR0005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus tage="SAS0005"
/note="Pfam match to entry PF02518 HATPase_c, Histidine
kinase-, DNA gyrase B-, and HSP90-like ATPase, score
103.9, E-value 3.4e-28"
5538. .5558
                         /locus_tag="SAS0004"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104182 TTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="SAS0005"
/note="P800154 E1-E2 ATPases phosphorylation site."
5727. .6239
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                                                                                                                                                                                                                    ≖.
⊘
                                                                                                     /locus tag="SASO004"
/note="PS00617 RecF protein signature
                                                                                                                                                                                          locus tag="SAS0004"
note="PS00618 RecF protein signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125.6; DB 1;
Pred. No. 2.4e-10;
0; Mismatches 379;
                                                                                                                                                                                                                                                                                                                            /locus_tag="SAS0005"
/EC_number="5.99.1.3"
                                                                                                                                                                                                                                                                      /locus_tag="SAS0005"
5037. ..6968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENRRQFIEDNAVYANLDF"
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                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1/transl_table=
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Best Local Similarity 50.9%;
Matches 413; Conservative
                                                                                                                                                              4848. .4901
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'protein id="CAG41776.1"
'dx ref="G1:49243159'
'translation="WILMILGLENYRNYDEVTLKCHPDVNILIGENAGKTNLLESIY
'translation="WILMILGLENYRNYDEVTRYCHPDVNILIGENAGKTVNLLESIY
FLALAKSHRTSNDKELIRFNADYAKIEGELSYRHGTMPLTMFITKKGKQVKVNHLEQS
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NNYLKQLQLGQKKDLTMLEVLANQSEQISTRFIDMELGQISAVYLNDLAQVQILIKQK
NNYLKQLQLGQKKDLTMLEVLANQSFAEYAMKVTDKRAHFIQELESLAKFIHAGITINDK
EALSLAYLPSLKFOYAQNEAARLEETHSILSDNMQREKERGISLFGFPHRDDISFDVNG
MDAQTYGSQCQQRTTALSIKLAEIELNNIEVGEYPILLLDDVLSELDDSRQTHLLSTI
QHKVQTFVTTTSVDGIDHEIMNNAKLYRINQGEIIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PÜLTGVNWLI QENELI CTATDSHRLAVRKLQLEDÜSENKNVI I PGKALAELAKIMSDN
BEBI DIT PFRASMYULFKVGNVPRI SRILLEGHY PDYTRLEPENYEIKLSI DNGEFYHAID
RASILLAREGGNNVI KLSTGDDVVELSSTSPET GTVKERVDANUVEGGSLKI SFNSKYM
MDALKAI DNDEVEVEFFGTMKPFILKPKGDDSVTQLILPIRTY"
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GVRETRRGKKLEHQDRIDIPELPEDAGSFLIIHQGEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTGSDSB1918111PKTVDGED1VN1SETGSVVLPGRFFVD11KKLPGKDVKLSTNEQ
FQTL1TSGHSBFNLSGLDPDQYPLLPQVSRDDA1QLSVKVLKNVIAQTNFAVSTSETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MMEFTIKRDYFITQLNDTLKAISPRTTLPILTGIKIDAKEHEVI
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/note="Pfam match to entry PF02463 SMC_N, RecF/RecN/SMC N
terminal domain, score -21.4, E-value 2.5e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="SAS0002"
/note="Pfam match to entry PF02767 DNA pol3_beta_2, DNA
polymerase III beta subunit, central domain, score 222.4,
E-value 7e-64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1912. .5024
/locus_tag="SAS0004"
1912. .5024
/locus_tag="SAS0004"
/note="Ortholog of S. aureus MRSA252 (BX571856) SAR0004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus tag="SAS0003"
note="Ortholog of S. aureus MRSA252 (BX571856) SAR0003"
                                                                                                                                                                                                                                                                                                                      note = "Ortholog of S. aureus MRSA252 (BX571856) SAR0002"
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                                                     locus tag="SAS0001"
rocte="PS00017 ATP/GTP-binding site motif A (P-loop)."
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/notes="Pfam match to entry PF02768 DNA pol3_beta_3, DN
polymerase III beta subunit, C-terminal domain, score
209.8, E-value 4.4e-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus tag="SAS0002"
/note="Pfam match to entry PF00712 DNA_pol3_beta, DNA
polymerase III beta subunit, N-terminal domain, score
224.5, E-value 1.6e-64"
protein, score 681.8, E-value 3.5e-202"
                                                                                                                                                                                                                                                                                                                                                                                                        producE="DNA polymerase III, beta chain"
protein id="CAG41774.1"
db_xref="GI:49243357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="conserved hypothetical protein"
protein id="CAG41775.1"
db_xrefe="G1:49243358"
                                                                                                                                  locus tag="SAS0001"
note="PS01008 DnaA protein signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus tag="SAS0003"
3670. .3915
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156. .3289
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EC_number="2.7.7.7"
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                            4182 TTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT 4123
                                                                                      1122 GGGTACAACTGAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 4063
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87 TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
                                                                                                                                                                                 TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
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                                                                                                                                                                                                                                              GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCCAGATTTAATTATTGCTGATAATAA
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                                                           147 AGGIACTACGAAAGIACCIAAACACCCIAAACGIGIIGIIGIICTIGAGIAIICAITIGI
                                                                                                                        TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAA
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Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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strain:MW2, section 1/10.
AP004822 BA000033
AP004822.1 GI:21203164
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                                                                              GTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGGATAAGAAAATTGAAGAATATA
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                    TTTCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAAACAATTTCAAAAGCTTTAG
                                                rircracrdaracagrrrrcaaarrcaaadaracaacraagrraargeggaaagcrrrad
                                                                                                                                           AAAAAGA---AATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTGCTAAAT
                                                                                                                                                                                                      CAGGITTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT
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0; Mismatches 379;
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Matches 413;
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                            Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
                                                                                                                           Direct Submission
Submitted (06-MAR-2002) Director-General, Biotechnology Center,
Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3461-1933, Pax:81-3-3481-8424)
Location/Qualifiers
1. 290250
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1. Corganiam="Staphylococcus aureus subsp. aureus MW2"
1. Corganiam="Staphylococcus aureus subsp. aureus MW2"
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104949 TCCGT----GCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGTGAAATCTTAAATG 104893
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R.
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Pred. No. 7.2e-10;
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/organism="unknown"
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EWITALTHOSLINGI IDAYRHDYHAYNPOROINVAARNBOMLEGSTLÄTRQAETRYQD
AYTLRCI PQIHGASPQVPYVKQQLEPERNAANDNPLI FERMIETSYILTRQDE TRYQD
APALDHLKLGVSELANVSERRLERLVNPOLNODLPARLSPEPCLQSGAMIMQYAAASI.
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RLNTLLKGHSGATLELVRQLQFFINERIIPIIPQGSLGASGDLAPLSHLALALIGEG
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ARFVYLTNEGAQLERALMNYMI TKHTTQHGYTEMMVPQLVNADTMYGTGQLPKFEEDL
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RLHQFDKVEMVRFEQPEDSWNALEEMTTNAEA I LEELGLPYRRVI LCTGDI GFSASKT
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/transl_table=11
/producE=seryl-tRNA synth
/protean_id="BAB93874.1"
/db_xref="G1:21203173"
                                                                                                                        /protein_id="BAB93873.1
/db_xref="G1:21203172"
                                        note="ORFID:MW0008"
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                                     361 ACAAAAA----TAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTAAAAGCTG 414
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                                                                                                             TITCTICAGAAGAATGGCAAAAGAACTIGITGAATTATCTAAGAAAGATAGTAAAAAAG 997
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
Kosen, C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 604 18-MAY-2004;
Location/Qualifiers
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                                                                                                                               TCGCAAGTGAAAGTATGGCAGAAGATTTAGAAAAATTGCAGAAAAAGCAAAATAAAAT
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               CTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTG
                                                             TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA
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llarity 53.2%; Pred. No. 7.2e-10;
Conservative 1; Mismatches 247;
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Sequence 604 from patent US 6737248.
AR556042.1 GI:53927259

    .2115
    /organism="unknown"
    /mol_type="genomic DNA"

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Unclassified.
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AR536042
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                                                                                                                                                 20283 AAGAAGAATCAAAAGAAGATACGAAAAAGAAATGATTCCTGTGGAACATGCAATGGGTA 20224
                                                                                                                                                                                                                          20223 AAACAGAAGTTCCTGCTAATCCAAAACGTGTAGTCATTTTAACAAATGAAGGTACTGAAG 20164
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                                       TAAGTGTAATTGGCTTATTGTTTTTAATTGCAACTGCAGCATGTGGAAATAATAGTT
                                                                          TATTIGIATITITATIAGCCTTTTCACTGCTTTTAAGTGCTTGTGGAAAATCAAATACGA
                                                                                                                CAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTA
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LOCUS CP000001 Accession CP000001

Sequence split into 53 fragments Fragment Name Begin Er CP000001_00

RESULT 40 CP000001 06/c WPCOMMENT

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17295 AAAAAGATGGCCAAAAGGTTTTAGCTGCTTACGATAAACGTATGAAAGATTTAAAAGCTA 17236
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                                   .7526 GGTATCCACATATTAAACATAAATGAAAGATGTAAAAGTTGTTGGTGATGAAGGACAAG 17467
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Search completed: August 26, 2005, 05:54:16 Job time : 4645 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

Copyright

- nucleic search, using sw model

OM nucleic

Run on:

ACA21545 AAV74915 ABT15032 972 3211 990 999 999 999 7745 796 900 900

2

ADF43555 ACC48531 AAV74549 ACA22139 ACF70890 ACF74610 AAH54418

ACF67367_39 ACF65388_08

ACA32751

25860 110000 110000

8780412

hits satisfying chosen parameters: 4390206 segs, 2959870667 residues

Total number of

Searched:

seq length: 0 seq length: 200000000

Minimum DB s Maximum DB s

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

US-10-724-972A-2580 1008

Title: Perfect score:

Sequence:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Geneseq 16Dec04:* geneseqn1980s:*

Database

geneseqn1990s:*

geneseqn2001as: geneseqn2000s

Aca21545 Prokaryot
Aaa69530 Exaphyloc
Aca16735 Prokaryot
Aav74915 Staphyloc
Abib362 Staphyloc
Adf4355 Staphyloc
Adf4355 Staphyloc
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Adf4355 Staphyloc
Aca22139 Prokaryot
Ac77610 Staphyloc
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Ac832731 Prokaryot
Ac832731 Prokaryot
Ac837335 DNA encod
Ac8713735 DNA encod

ALIGNMENTS

ADS03285 standard; DNA; 1008

BP.

29-JUL-2004.

01-DEC-2003; 2003US-00724972.

08-NOV-1997;

Doucette-Stamm L,

WPI; 2004-580138/56. P-PSDB; ADS07057.

Staphyloc Pathogen

Prokaryot Adf30765 Bacillus

Abt15015 | Aca20079 |

Aav74666 Staphyloc Aav76867 Staphyloc Abn92560 Staphyloc

ABN92560

156.4 149.4 143.2 (without alignments)
9265.682 Million cell updates/sec 1 ggagtggaatcagtgagagg.....gtaaaaaagataataagtaa 1008 August 25, 2005, 23:38:01 ; Search time 644 Seconds

ADS03285;

04-NOV-2004 (first entry)

Staphylococcus epidermis polynucleotide segid 2580.

antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system; gene; ds.

Staphylococcus epidermidis.

US2004147734-A1.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:*

geneseqn2002bs: geneseqn2001bs:

geneseqn2004bs:

10: 11: 13:

SUMMARIES

97US-0064964P. 98US-00134001. 99US-00450969. 13-AUG-1998; 29-NOV-1999;

Ads03285 Staphyloc

Description

Aca47084 Prokaryot

ADS03285 ACA47084

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Query Match Length

Result No.

ACC48532 ACA19774 AAS54519

AAS51822 AAT80398

ACF74986

ACA47237 ACC48534 AAT83786

> 309.8 269.2 265.6 264.6

336. 309. AAS51612

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AAS54387

(DOUC/) DOUCETTE-STAMM L. (BUSH/) BUSH D.

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Acc48532 Staphyloc Aca19774 Prokaryot Acf74986 Staphyloc Aac1822 Staphyloc Aac1822 Staphyloc Aac1823 Staphyloc Ac47237 Prokaryot Acc46534 Staphyloc Acc46534 Staphyloc Aac543612 Staphyloc Aac5431612 Staphyloc

New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.

Claim 5; SEQ ID NO 2580; 741pp; English.

The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any

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of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an S. epidermidia polypeptide; an isolated nucleic acid producing an uncleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleotide devoke and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially a repearation of an S. epidermidis infection; a recombinant or substantially a vaccine composition for prevention or treatment of an S. epidermidis infection; a readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome and/or plasmids of commercial importance; a computer based system for identifying medium thating fragment of the Staphylococcus and identifying an expression medulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression medulating fragment of the Staphylococcus genome and/or plasmids of an Staphylococcus patermis protein of the invention. This seminance and compositions of the present invention are useful for the diagnosis, infection, This seminance and composition as encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes and encodes as an encodes as an encodes as an encodes as an encodes as an encodes as an encodes and encodes as an encodes as an 
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llarity 100.0%; Pred. No. 3.3e-175;
Conservative 0; Mismatches 0; Indels 0;
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Matches 1008; Conserv
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960 960 720 780 840 840 900 900 the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(I) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the invention relates to an isolated nucleic acid comprising any one of CTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATTT TTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAA TTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTTCTTCAGAAGAATGGCAAAA CAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTAAAGGTTTA AGTAAGTATCTTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAAT <u>AGTAAGTATCTTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAAT</u> CCTGAGCGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAA CTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATT CAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTAAAGGTTTA Zyskind JW; Xu HH; S New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. GAACTTGTTGAATTATCTAAGAAAGATAAAAAAAAAAAGATAATAAGTAA 1008 ds; prokaryotic essential gene; cell proliferation; ∄,≅ Ohlsen | Forsyth | Haselbeck R, Yamamoto R, Claim 14; SEQ ID NO 34954; 1766pp; English. Malone C, Carr GJ, BP 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 ACA47084 standard; DNA; 993 gene Staphylococcus epidermidis (first entry) (ELIT-) ELITRA PHARM INC. Prokaryotic essential Zamudio C, Trawick JD, 2003-029926/02. drug design; gene. WPI; 2003-029926/ P-PSDB; ABU43214. WO200277183-A2 19-JUN-2003 03-OCT-2002 Antisense; ACA47084; 781 841 901 661 721 721 781 841 901 961 υŗ, Wang ACA47084
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cc antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway compared for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies compared in which a proliferation-required gene or its gene product lies compound's acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in the strains of a culture or collection of compound of an organism. The antisense mucleic acids required for cellular proliferation to isolate candidate molecules for rational compound acts of acts and activity. The sequence is one of the target condition in cells other than S. aureus, S. typhimurium, conditions proved form part of the printed specification, but was obtained in cellectronic format directly from WIPO at compound the condition of the printed proved conditions or this parent did for the printed specification, but was obtained in cells sequence and the printed proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved proved 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.5%; Score 993; DB 8; Length 99 Best Local Similarity 100.0%; Pred. No. 1.9e-172; Matches 993; Conservative 0; Mismatches 0; Indels
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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
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                                                                                                                                                                          CCTGTATIGGAAGAATTAAACGCTGTGAAAATCAACGTGTTGATTTTAGACCGTGAC
                                                                                                                                                                                             CCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGAC
601 GCTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGT
                                     AAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATG
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                                                                                                                         TTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAAAT
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              sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, in combination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop diagnostic
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the following and the control of a cell of the muties and the capture of the muties are comprising a promoter operably linked to the mutiest acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mutiest acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated concluded are:

(2) polypeptide or its fragment whose expression is inhibited by the antisense concleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation and that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture compound strains in which the estent compound that inhibits proliferation of compound activity; (12) determining the extent concounts or (13) identifying the target of a compound that inhibits the
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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              identifying proceins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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The antisense nucleic acids are useful for
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Pred. No. 1.5e-94;
0; Mismatches 260; Indels
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Best Local Similarity 73.6%;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes chair use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia chemically staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, consecutation of potential new targets for antibiotic consecut in proliferation of potential new targets for antibiotic consecut in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can compound in rational drug discovery programmes. The proteins can succeed an used to screen compounds in rational drug discovery programmes. The nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic collular proliferation protein. Note: The sequence data for this patent coll cornic format directly from WilbO at celectronic format directly from WilbO at celectronic format directly from WilbO at
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                                                                 TATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAATGGCAAAAGAACTTGTTGAAT
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CTGTATGGAAGAAATTAAACGCTGTGAAAATCAACGTGTTGATATTTAAGACCGTGACT
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GTAATACGGATAATTCGAGTAAAAAAGAATCATCAACTAAAGATACTATTTCGGTAAAAG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein, useful as a vaccine for treating or infection, specifically an infection caused by
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                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
enzymatic assay; antibiotic target; gene; ds.
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Pred. No. 8.5e-93;
; Mismatches 256;
985 GTTGAATTATCAAAAAAAGAACAAAAGTAA 1014
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larity 73.5%;
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es 711; Conserv
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1031 AAAAAGA 1037
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301 ATTAGTAAATTAAAACCGGATTTAATTATCGCTGATAGCAGTAGACATAAAGGTATTAAT 360
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46 TTATTGTTTTGTTTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGT
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                                                                                                                                                                                                                                                                                                                                                                    Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus DNA for cellular proliferation protein #239.
                                                                                                                                                                                        BP.
                                                                                                                                                                                        AAS51822 standard; DNA; 927
                                                                                                                                                                                                                                                                                 (first entry)
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13-FEB-2002

AAS51822;

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Indels

247;

52.8%; Score 531.8; DB 73.4%; Pred. No. 4e-88; ive 0, Mismatches 2

680; Conservative

Local Similarity

Query Match Matches

DB 4; Length 927;

285

180

405

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361 AAAGAATTAAACAAATTGCACCAACATTATCATTAAAGAGTTTTGATGAACTACAAA 420

21-MAR-2001; 2001WO-US009180

WO200170955-A2

27-SEP-2001

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify attribodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can encise acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic collular proliferation protein. Note: The sequence data for this patent directly from mathor of the printed specification, but was obtained in
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                                                                                                                                                                                         Trawick JD,
                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                         Wall
                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 4404; 511pp; English
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                                                                                                                                                                                           Zyskind JW,
            23-MAY-2000; 2000US-0206848B:
26-MAY-2000; 2000US-0207737P:
23-OCT-2000; 2000US-0242578B:
27-NOV-2000; 2000US-0253625P:
22-DEC-2000; 2000US-0253635P:
16-FEB-2001; 2001US-0269308P:
                  2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
2000US-0253625P.
2000US-0191078P
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus Gene #4 encoding cDNA sequence
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                                                                                                                                                                                                                                                                                                         GAAGAAATGGCAAAAGAACTTGTTGAA
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vaccine; diseal
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expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptide can be used to isolated candidate compounds that bind and inhibit the activity of the polypeptide. Such compounds can be used as anti-bacterial compounds. The polypeptide may also be used as an immunogen to vaccinate an animal for protection against Staphylococcus
                                                                                                                                                                                                                                                                                                                                          TAATTCGTTCAACAACTTGCTAAAGCTTTAAATAAAGANAAAGAAGGCGNNAAACGTC
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                                                                                                                                            Sequence 2247 BP; 704 A; 397 C; 307 G; 802 T; 0 U; 37 Other;
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Pred. No. 2.5e-52;
0; Mismatches 229;
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0
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                                                                               CGTATCGTTGTTTAGAGTACTCATTTGCAAGGTTGCATTANCAGCATATAGCCGTTANA
                                                                                                                                                        CGTGTTGTTGTTCTTGAGTATTCATTTG--TTGATGCGTTAGTTGC-TTTAGATGTTAAA
                                                                                                                           CC-TGTTGGGATAGCGGATGATAACAAAAAAAAAATCGTATTAAAAACCATTAAGAGATAA
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGTGGGGACNGATGAGAGGTCTAAAAACTTTTAGTATATTGGGATTAATAGTTGCCTTA 772
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                                                                                                                                                  Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - us. isolate antimicrobial compounds, and in vaccines against S. aureus
                                                                                                                 DNA encoding 3 Staphylococcus aureus proteins of unknown function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain WCUH29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2247 BP; 704 A; 397 C; 307 G; 802 T; 0 U; 37 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicholas
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Ward JM;
                                                                                                                                                                                                                                                                                                              complement (1212. .1445)
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Rosenberg M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW27819, AAW27820, AAW27821
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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complement(1705.
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AAT83786 standard; DNA; 2247 BP
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Reichard RW,
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                                                                                                                                                                                                                                                       Staphylococcus aureus.
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tes 580; Conserv
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Matches
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
compound acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
complypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
complypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operor required for
compound that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
compound a gene required for cellular proliferation of an
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
compound's crivity; (12) identifying the target of a compound that inhibits the
compound's proliferation of an organism. The antisense nucleic acids are useful for
conditional proliferation of solate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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0; Mismatches 112; Indels 12; Gaps
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                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 525 BP; 200 A; 66 C; 96 G; 163 T; 0 U; 0 Other;
                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                     Claim 14; SEQ ID NO 35107; 1766pp; English.
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                                                                                     Malone C,
Carr GJ,
06-MAR-2002; 2002US-0362699P.
                                        ELIT-) ELITRA PHARM INC.
                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                          WPI; 2003-029926/02
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                                                                                        Wang L,
Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA05. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-raphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain straphylococcal infection. They can also be used to develop diagnostic
                             302 ATTATAAATCTGTTGGTGCTCGTAACAACCCAACTTAGAAGAAATCAGTAAATTAAAAC
                                                                                    362 CAGATITAATTATGCAGATAGTAACAGACACAAAGGTATTTACAAAGAATTAAGTAAAA
                                                                                                                                                     AATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAAC
                                                                 CAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAAAA
                                                                                                                                422 TTGCTCCTACGATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcal surface-exposed immunogenic polypeptide DNA
                                                                                                                                                                                                  482 TIAAAACAATITCAAAAGCITTAGGIAAAGAAGAAGAAGGIAA 524
                                                                                                                                                                                                                      /note= "No start codon"
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983. 1960
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial; vaccine; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "SEIP"
                                                                                                                                                                                                                                                                                                                  ACC48534 standard; DNA; 2957 BP.
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                                                                                                                                                                                                Gaps
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                                                                                                                            Length 2957;
                                                                Sequence 2957 BP; 1160 A; 381 C; 512 G; 904 T; 0 U; 0 Other;
                                                                                                                                                                                                Indels
                                                                                                                         Score 269.2; DB 8;
Pred. No. 4.6e-40;
0; Mismatches 433;
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                                                                                                                                Query Match
26.7%;
Best Local Similarity 55.4%;
Matches 545; Conservative
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes there were their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bacherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, seruginosa and Enterococcus feacails. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins can encompounds in rational drug discovery programmes. The nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed opecification, but was obtained in calcetronic format directly from WIPO at
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26.3%; Score 265.6; DB 4; Length Sest Local Similarity 57.8%; Pred. No. 1.9e-39;
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P-PSDB; AAU36528.
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prokaryotic cellular proliferation gene, antibiotic; drug design.

Staphylococcus aureus

Antisense; ds; antibacterial;

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can entisense nucleic acids equence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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Xu HH;
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P-PSDB; AAU33753.
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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23-MAY-2000;
26-MAY-2000;
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Yamamoto RT,
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enzymatic assay; antibiotic target; gene; ds.
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                       Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          26.2%; Score 263.8; DB 8; 55.3%; Pred. No. 4.2e-39; iive 0; Mismatches 427;
NO 4189; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 536; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprise providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune fragments are useful for the manufacture of a contraction of antibodies is useful for the manufacture of a medicament of preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation of against subject to the manufacture of a medicament of cor treating or preventing staphylococcal infections or colonisation of against subject on a medicament of antibodies is useful for the manufacture of a medicament of articles and imaging purposes Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral
                                                                        916
                                     841
                                                                                                            901
                                                                                                                                                                               Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; auto-immune disease; HIV; hepatitis; gene; ds.
TAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAAGATCCTG
                                   ragccactgacgaaaaacgacaaaaa-----ragaacgaaatrcattgatcctgcag
                                                                          TATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTAT
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                                                                                                                                                 GGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAATGGCAAAAGAACTTGTTGAATTAT
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Hafner M;
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Dryla A, Weichhart T,
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Etz H,
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3, Vytvytska
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(e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This polynucleotide sequence represents staphylococcal DNA relating to the method for identifying and producing pathogen specific antigens of the
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                                                                                                                                                                                                          108 AGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAA
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                                                                      0 Other;
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                                                                      T; 0 U;
                                                                                             Score 263.2; DB 8;
Pred. No. 5.4e-39;
0; Mismatches 408;
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                                                                      C; 210
                                                                                             Query Match 26.1%;
Best Local Similarity 55.9%;
Matches 524; Conservative 0
                                                                       Sequence 957 BP; 383 A; 116
                                             invention
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the follamination of a cell. Also included are:

the follaminations bequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated carification whose expression is inhibited by the antisense carification or its fragment whose expression is inhibited by the carification or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway captured for proliferation, or that has an activity against a biological pathway captured for proliferation, or that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or undersexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the cypical for proliferation of an organism. The antisense nucleic acids required for proliferation of an organism or screening for homologous nucleic acids required for fearly additional proliferation or the proper candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target probaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
AAGTATGGCAGAAGATTTAGAAAAATTGCAGAAAAG 952
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Yamamoto R,
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                ACA20079 standard; DNA; 960
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                                                                                                                                             Score 263.2; DB 8;
Pred. No. 5.4e-39;
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electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                             Query Match 26.1%;
Best Local Similarity 55.9%;
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CCTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTAATAAACCATTAAGAGATAAA 294
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                                         CCGGTGGGCATCGCAGATGACAAAAAAGATATGATTAAAAAAGCTTGTCGGCAGCTCC
                                                                                                                                                                                                                                                 694 TIGAAGCCTGATTTAATCATCGCTGACGCTGAGCGCCATAAAAACATTTATAAACAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for generating an expression library of polynucleotides integrated by homologous recombination into the genome of a competent gram-positive bacterium host cell. The method comprises: (a) providing a non-replicating linear integration cassette; and selecting or screening for host cells that produce the polygeptides of interest. The cassette comprises: (a) a polymucleotide encoding one or more polypeptides of interest; (b) a 5' flanking polynucleotide segment comprises of interest; (b) a 5' flanking polynucleotide segment comprising a second homologous region located in the 3' end of the segment; and (c) a 3' flanking polynucleotide segment downstream of the polynucleotide of (1) and comprising a second homologous region located in the 5' end of the segment. The first and second homologous regions are at least 80, 85, 90 or 1500 bp, each of which has a sequence identity of at least 80, 85, 90 or 1500 bp, each of which has a sequence identity of at least 80, 85, 90 or 59-100* with a region of the host cell integration cassette; and con-replicating ilnear Gram-positive host cell integration cassette; and con-replicating an expression library of polynucleotides integrated by homologous recombination into the genome of a competent Gram-positive characterium host cell. The present sequence represents a Bacillus subtilis strain which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generating an expression library of polynucleotides by introducing the linear integration cassette into the host cell and selecting or screening for host cells that produce the polypeptides of interest.
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                                                                                                                                                                                                                            Bacillus subtilis strain MB1510 integration region DNA SEQ ID NO:20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5718;
                                                                                                                                                                                                                                                                        expression library, Gram-positive bacterium host cell; non-replicating linear integration cassette; gene; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 357; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
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Pred. No. 1e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; SEQ ID NO 20; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hansen
                                                                             ADF30765 standard; DNA; 5718 BP
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Matches 488; Conservative
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Best Local Similarity
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The be used in a vaccine composition against S.aureus infection of S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock for recombinant production of the polypeptides. The new DNA sequences can be used their fragments) are useful as primers or probes for isolating computer computer.
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/note= "these bases represent a line of missing text in
the sequence listing in the specification. They are
included to maintain the nucleotide numbering given in
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stored on computer readable medium and used in the production of anti-
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                                                                                                                       the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1239-1240; 3271pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH,
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of saureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (and their fragments) are useful as primers or probes for isolating nomologues of any of the S.aureus DNA sequences contained on the computer
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                                                                                                                                                                                                                                                                                Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fannon MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon PJ,
                                                                                                                                                                                                                                                Staphylococcus aureus contig SEQ ID #2556.
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                                                                                                                                 AAV76867 standard; DNA; 242
                                  361 ACAAAAGTAAGGT 373
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                toxic shock syndrome; ds
987 TAGTAAAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
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867 ATTAAACGCTGTGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATC GTTGAATGCAGTTAAAAAATAATCGCGTGGATATTGTTGACCGTGATGTTTGGCCAAGATC

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cenceding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated control of antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contineration; (7) identifying a gene in an operon required for proliferation or that has an activity against a biological pathway or equired for that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an entibiotic; (10) profiling a compound that inhibits strains in which the gene compound that inhibits the compound; activity; (11) a culture comprising strains in which the gene compound; activity; (11) a culture comprising strains in which the gene compound; activity; (11) a culture comprising strains in which the extent compound; a compound that inhibits the compound; or 13) identifying the target of a compound that inhibits the contiferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are squaired.
                        CCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAATGGCAAAAAGAACT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
CCGTGACTTATGGCCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACT
                                                                                                                                                                                                                                                                                                                                              Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                       TGTTGAATTATCTAAGAAGATAGTAAAAAAAGATAATAAGTAA 1008
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Forsyth RA,
                                                                                                         rcrrcaarrarcraagaragaragraaaaagaraaragraa 183
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 30706; 1766pp; English.
                                                                                                                                                                                                                                                                                                            Prokaryotic essential gene #24493.
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                   ACA42836 standard; DNA; 897
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                    design; gene
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25-OCT-2001; 2
08-FEB-2002; 2
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Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermidis; open reading frame; ORF; bacterial infection; gene therapy; gene; ds.
                                                        CAACCTAACTTAGAAGAATCAGTAAACTTAAACCAGATTTAATTGCTGATAATAAT 387
                                                                                          181
                                                                                                                             447
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80
                                                                             CAGCCAAACTTAGAAAATTAGTAAAATTAAAACCGGATTTAATTATTATTAGTGATAGCAGT
                                                                                                                                                  388 AGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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Best Local Similarity 98.2%; Pred. No. 7.7e-20;
Matches 160; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                               ABN92560 standard; DNA; 183 BP.
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97US-0064964P.
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P-PSDB; ABP40015.
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08-NOV-1997;
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Zyskind JW; Xu HH;

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                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                              IGITGITCITGAGIATICATITGITGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 GATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 TGTCGCAGATGACATGATAAAACCCGTATTCTGCAAAAAGTACGCGATAAAGTGCAGCC
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cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGATAAGAAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 TAAGCAGGATATTGCGG----ACATCGCCAAAACGTTACCGAAAGGGAAAAAAGCGAT
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                                                                                                                                                                                                                            Score 156.4; DB 8 Pred. No. 1.8e-19;
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Best Local Similarity 51.9%;
Matches 454; Conservative
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The invention describes a method of monitoring differential expression of content and a first Bacillus cells relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes is isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining captured from Bacillus cells in observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for measuring the same genes or more second Bacillus cells. The method is useful for monitoring captures as identifying possible functions of unknown open reading frames and controring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, in expression at stress or other physiological provocation. Extensive follow cup characterisation is unnecessary, when one spot on an array equals one cone open reading frame, since sequence information is available. This sequence represents a genomic sequence information is available. This sequence represents a genomic sequence information is available. This sequence the printed specification, but was obtained in electronic format contents from WIPO at ftp. WiPo.int/Published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
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864 AGTCCAAGACTTTGTAACGAAATCCGCCAAATAA 897
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27-MAR-2001; 2001US-0279526P.
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51.8%;
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screening

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

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Wang Wall

(ELIT-) ELITRA PHARM INC Zamudio C, Trawick JD, 2003-029926/02 P-PSDB; ABU17675

2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P.

06-SEP-2001; 25-OCT-2001; 08-FEB-2002; 06-MAR-2002;

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                                                      TTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAAC
                                                                                 TCAAAGGGTATACTTCAGTCGGTTCGCGCCCCAGCCAAGCTTTGAAAAATTGCTTCTT
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide for its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding cholypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway to which the test compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or treased or treased or underexpressed; (12) determining the extent to the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibite the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K. pneumoniae or P. aeruginosa. The present sequence is one of the target
prokaryotic essential genes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 GAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTGAGTATTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 4.7e-17;
0; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 9415; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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55.0%;
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Matches 308; Conservative
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Bacillus anthracis

03-OCT-2002

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Gaps

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Length 321;

212 251

92

32

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

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coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. WIPO.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                            TGATAACAAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAAT 371
                                                                                                                                                                                                                                                                                                           271 AATAAAAGATGAATTAGGAACTGAAAAAATTAAGAAAAATCCTAAACGTGTTGTTGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AATCAAGCACGAAGAAGTACTACGAAAGTACCTAAACACCCTAAAACGTGTTGTTCT
                                                                                                                                                                                                                                                                                                                                         TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                          rcarcecaccacraaaararaacaaagrcagraagagaraagagarrcagggggggaragaarc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prokaryotic essential gene antisense oligonucleotide #4605.
                                                                                                                                                                                                                        Score 128; DB 4; Length 32
Pred. No. 2.7e-14;
0; Mismatches 85; Indels
                                                                                                                                                                                             Sequence 321 BP; 83 A; 73 C; 36 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTGCTGATAATAATAGACACAA 395
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FSB-2002; 2002US-0362851.
06-MAR-2002; 2002US-0362699P.
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Similarity 67.8%;
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                                                                                                                                                                                                                                                       Conservative
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Trawick JD,
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19-JUN-2003
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drug design.
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Matches 179;
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Wall
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                   246
                                                                                                                                                                                                                                          486
                                                                                                                            307 caacaaccaaacrragaacaaarragccgrrraaaaccagarrraarrarcacagcrrca 366
 AAAGCTTTAGGTAAAAGAAGAAGAAGTAAAAAACGCTTAGAAGAACACGATAAGAAAATT
                                                                                                                                                                                                                                                                                      Staphylococcus aureus cellular proliferation inhibitory sequence #754
                                             AATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGT
                                                                       AATAAATGGGTAAATACAAAACAAAACCGAGTAAAGATGTTGTAGATGTCGGGACACGT
                                                                                                   AAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTGCTGATAAT
                                                                                                                                                         385 AATAGACACAAAGGTATTTATAAAGACTTAAATAAATTGCTCCTACGAT-----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prokaryotic cellular proliferation; antibiotic;
drug design.
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                                                                                                                                                                                                                                                                                                                                 GAAGAATATAAAAAAGAAAT 575
                                                                                                                                                                                                                                                                                                                                                          547 GCTGATGCAAAAGCAAAAT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                AAS49530 standard; DNA; 321 BP
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, 2000US-020648P.
, 2000US-020727P.
, 2000US-024578P.
, 2000US-025362P.
, 2001US-025362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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26-MAY-2000;
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Yamamoto RT,
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16-MAR-1999 (first entry)

AAV74915;

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an isolated containing the vector; (3) an isolated contained by the properties or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation; (8) identifying a compound that inhibits proliferation; (9) identifying a compound that inhibits proliferation or the biological pathway required for proliferation, or that that inhibits proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acis; (8) product is overaxpressed or underexpressed; (12) determining the extent of product is overaxpressed or underexpressed; (12) determining the extent of proliferation of an organism. The antisense nucleic acids required for callular proliferation in cells of a compound that inhibits the proliferation of an organism. The antisense modelic acids are useful for calcular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for proliferation to isolate candidate molecules for trional drug discovery programs, or for screening for homologous nucleic acids are useful for required for proliferation to isolate candidate molecules one of the format diacotic format directly from William William William William William Willi
                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                        Claim 1; SEQ ID NO 4605; 1766pp; English.
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standardise OS field)
                           WPI; 2003-029926/02
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AATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCT 0; Gaps Length 321; Score 128; DB 8; Length 32 Pred. No. 2.7e-14; 0; Mismatches 85; Indels Sequence 321 BP; 83 A; 73 C; 36 G; 129 T; 0 U; 0 Other; 12.7%; 67.8%; Best Local Similarity ov.ogatches 179; Conservative Query Match Best Local Similarity 132 ò

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212 251 211 AGAATATAGTTTTTGCTGATTATTTAGCAGCATTAGATATGAAACCTGTTGGTATTGCAGA 152 TGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTC 311 TGATGGCAGCACTAAAAATATAACAAAGTCAGTAAGAGATAAGATTGGGGCATATGAATC 92 271 AATAAAAGATGAATTAGGAACTGAAAAATTAAGAAAAATCCTAAAACGTGTTGTTATT TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGA 192 252 151 용 ઠે 줨 ઠે 유 ઠે

TGTAGGAACACGTAAGCAACCTAAGAAGAAATCAGTAAACTTAAACCAGATTTAAT 371 GGTTGGATCTAGACCGCAACCGAATATGGAAGTGATAAGTAAATTAAAACCGGATTTGAT 312 91

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372 TATTGCTGATAATAATAGACACAA 395 carriccagargrragcagacaraa 31

AAV74915 standard; DNA; 2115 BP AAV74915 ID AAV7 XX

541. .600
/*tsg= a
/*tsg= a
/*teg= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" Computer readable medium; vaccine; S.aureus infection; immunodetection; Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines. cellulitis, eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. Rosen CA; Fannon MR, Dillon PJ, Staphylococcus aureus contig SEQ ID #604. Location/Qualifiers Barash SC, 97EP-00100117. 96US-0009861P. (HUMA-) HUMAN GENOME SCI INC Staphylococcus aureus. Choi GH, WPI; 1997-374922/35. misc_feature 07-JAN-1997; 05-JAN-1996; EP786519-A2 30-JUL-1997 Kunsch CA,

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access meaning (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The collypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock of syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used to homologues of any of the S.aureus DNA sequences contained on the computer readable medium

Claim 1; Page 1535-1536; 3271pp; English.

Sequence 2115 BP; 787 A; 279 C; 363 G; 622 T; 0 U; 64 Other;

Gaps

9

Score 125.4; DB 2; Length 2115; Pred. No. 8.9e-14; 1; Mismatches 247; Indels 6;

12.4%;

Matches 289; Conservative

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Local Similarity

Query Match

32

AAGGCGAGAAGCGTCTGGAAAAGCATGATAAAATATTAGCGGAGATTAGAAAAAATTG 120 61

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300
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                                                                                                                                                                 301 argaagaacirgccaararcaarccaaaggriargarirriagccacrgagagaaaaagg 360
                                                                                                                                                                                                               361 ACAAAAA-----TAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTAAAAGCTG 414
                                                                                                                                                                                                                                                               rcaaagaraacaracritargacgrigaccgaaaraagriggirgaaarcaagggggarra 474
                                                                                                                                                                                                                                                                                                              TCGCAAGTGAAAGTATGGCAGAAGATTTAGAAAAATTGCAGAAAAAGCAAAATAAAAAT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; anti-HIV;
                                                                                                                                                                                                                                        TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA
                                                         121 AACAGAGTACGTTAAAATCTGCATTTCGGTATCTCAAGAGCAGGTATGTTAATTA
                                              ATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAA
                                                                                           698 GTGATGATGTTACTAAAGGTTTAAGTAAGTATCTTAAAGGACCTTACTACAATGAACA
                                                                                                                 CTAACGAACCTTCACTAAAAGAACTAGAAAAAAGATCCTGTATGGAAGAAATTAAAACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathogen specific antigen related staphylococcal DNA SEQ ID No 318
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                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma cool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the immunity. The hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament or against S. epidermidis. The antibody preparations may also against S. aureus or S. epidermidis. The antibody preparations may also consist in the specific antiposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This continue for identifying and producing pathogen specific antigens of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622
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Pred. No. 1.5e-13;
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50.7%;
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Tempelmaier B;

WPI; 2003-075410/07.

(CIST-) CISTEM BIOTECHNOLOGIES GMBH.

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Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody

Example 7; Page 210; 252pp; English.

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06-DEC-1999 (first entry)
                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents Staphylococcus aureus cbrA DNA. The cbrA protein is predicted to have a molecular weight of about 36.8 kD and, along with cbrB day423313 and cbrB. (A7442333), is thought to be involved in iron regulation, based on amino acid sequence homology with known iron regulations in burns, callulitis, eyelid infections which causes infections in burns, callulitis, eyelid infections, book poisoning, joint infections in neonatal conjunctivitis, eyelid infections, skin infections, infections, neonatal conjunctivitis, eyelid infections, skin infections, cargical wound infection, scalded skin syndrome and toxic shock syndrome. Staureus is increasingly becoming resistant to known antibiotics, with mathy strains generally being multiply drug resistant. Methicillin-resistant strains generally being multiply drug resistant. Methicillin-resistant serious infection control cantibiotics with many strains being multiresistant against virtually all antibiotics with the exception of the vancomption-type glycopeptide antibiotics. The protein may be useful to screen potential antagonists which could be used as antibiotics and it may be used as a vaccine to prevent or attenuate an infection caused by a member of the control caused the protein, or antibodies against it can be used in immunoassays to detect Staphylococcus in a biological sample. Probes
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                                         802
                                                                  775
743 ACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGTTCATAATGA
                                                                  716 TCCAACTTACATCTAAAGAAAGCATTCCATTAATGAACGCTGATCATATTTTGTAGTAA
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                                                                                                                                                                                                                                                                                                  Infection, detection, diagnosis, screening, antibiotic, resistance,
methicillin, MRSA, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus genes and polypeptides, vectors and methods
                                                                                                                                                                                                                                                                                                                                                                                                             /product= "S. aureus cbrA protein"
                                                                                              803 CAAACAAAGCAAGTTCTAACGAACCTTCACTA 834
                                                                                                                        776 AATCAGATCCAAATGCGAAAGATGCTGCATTA 807
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7. 999
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN GENOME SCI INC.
LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                          Staphylococcus aureus chra DNA
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                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
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P-PSDB; AAY42331.
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01-APR-1998;
07-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545 AAAAAGATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTGTTAACT
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                                                                                                                                                                                                                                                                              27 AATTITAAGTGTAATTGGCTTATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAATAA
                                                                                                                                                                                                                                                                                                                                          AATTAAAATGCTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     20;
                                                                                           Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;
                                                                                                                                                                                                                     0; Mismatches 380; Indels
                                                                                                                                                          Score 124; DB 2;
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCAGATCCAAATGCGAAAGATGCTGCATTA 813
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662 AİTTAĞGATTCAAACGIAATAAAGACTTACAAAACAAGTTGATAATGGTAAAGATATTA 721
                                                                                             258 ACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAAGAACC 317
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                                                                                                                                                                                                                                                                                                                             GTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATA 565
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                                                                                                                                                                                                                                                                                                                                                          ggajagajaajagangcigajagattacitajajaggatacgatajajaggaggaggagtac
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                                                                                                                              327 GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTAGTGATAATAA
                                                                                                                                                                                                                                                               TTTCGATGGAGATTATAATGAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
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                                                                267 TCGTATTATAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA
                                                                                                                                                                                               TAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
                                                                                                                                                                                                                                                                                           trictacteatacagitttcaaattcaaagatacaactaagttaatggggaaagcttaag
TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial; immunostimulant; vaccine; vaccine; Staphylococcus aureus infection; infection prevention; infection attenuation; gene; ds; cbrA.
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/*tag= a
/product= "cbrA"
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(ATCC 202108) genomic DNA including the novel cbrA gene that codes for a 30-amino acid protein (see AAY18124) of predicted mol. wt. 36.8 kDa. The gequence was obtained from overlapping clones BTACA44 and BTAGA54, which span a single operon containing the cbrA, cbrB and cbrC genes (see AAI1889-91). CbrA shows sequence homology to known genes involved in circum regulation. The invention provides 11 novel genes (see AAX1887-92) of S. aureus and the polypeptides they encode (see AAY1817-27). Also provided are vectors, host cells, antibodies and hybridomas. The and antagonists of S. aureus polypeptide activity, and to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. Antagonists of cbrA may be useful as antibiotics to treat infections of S. aureus and other Staphylococcus spp. Also provided are novel vaccines for the prevention or attenuation of useful for generating probes and primers, and in the recombinant constraint constraints.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AGGIACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 GGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTITAAGTGTAATTGGCTTATTGTTTTTAATTGCAACTGCAGCATGTGGAAATAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTAAAATGCTTGTTACGCTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Staphylococcus nucleic acid molecules, used to develop products for the diagnosis, prevention and treatment of Staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                      CbrA gene; infection; therapy; diagnosis; vaccine; antibiotic; iron regulation; 88.
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Pred. No. 1.5e-13;
0; Mismatches 380; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;
                       Staphylococcus aureus iron regulation gene cbrA.
                                                                                                                                      Location/Qualifiers 7. .999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 24; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                      HUMAN GENOME SCI INC.
LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                     98US-0078682P.
98US-0080296P.
98US-0084674P.
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50.7%;
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                                                                                                         Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                      Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-562101/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY31824.
                                                                                                                                                                                                                                                                                                       20-MAR-1998;
01-APR-1998;
07-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Simpson AJG,
                                                                                                                                                                                                                                                                        19-MAR-1999;
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Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trcaaataaacaatcatcigataacaaagataaggaaacaacircaattaaacatgcaat 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTATTGCTGATAATAA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 TGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT 377
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                                                                                                                                                                                                                                                                                                                    The invention describes a new isolated nucleic acid molecule comprising:
a sequence that is 95% identical to a fully defined sequence having 586-
2226 bp, or its complement; or a sequence encoding a polypeptide having a
fully defined sequence comprising 136-691 amino acids, or its complement.
The gene is Staphylococcus aureus gene. The nucleic acid is useful for preparing a vaccine against infection caused by Staphylococcus aureus.
The methods are useful for preventing or attenuating an infection caused by a Staphylococcus, detecting Staphylococcus aucleic acids in a biological sample obtained from an animal, and detecting Staphylococcus antibodies in a biological sample obtained from an animal. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 GGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGTGCCAC 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                               gene, useful for preparing a vaccine against
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12.3%; Score 124; DB 10; Length 999;
Best Local Similarity 50.7%; Pred. No. 1.5e-13;
Matches 412; Conservative 0; Mismatches 380; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encodes Staphylococcus aureus cbrA protein.
                                                                                                                                                                                                                           New Staphylococcus aureus gene, useful for
infection caused by Staphylococcus aureus.
                                                                                                                                                                                                                                                                                    Claim 1, SEQ ID NO 15; 61pp; English.
98US-0080296P.
98US-0084674P.
99WO-US006199.
                                                      15-JAN-2002; 2002US-00830217.
                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                 Choi GH;
                                                                                                                                                                      2003-897737/82.
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01-APR-1998;
07-MAY-1998;
18-MAR-1999;
                                                                                                                                   Simpson AJG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SAO2. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisers. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or problination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop diagnostic asseays
  604
                                      CAGGITIGCTIGCTCCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTT
                                                                                                                                                                                              743 ACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGGGGTATGTTCATAATGA
                                                                                                                                                                                                                                722 recaactracarcraaagaaagcarrecarraargaacgergarcararrirreragaa
545 AAAAAGATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTGTTAACT
                                                                            rccgr----gcrgarcaracaagaarrrargcrggrggarargcrggrgaarcrraaarg
                                                                                                                662 ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor; antibacterial; vaccine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcal surface-exposed immunogenic polypeptide DNA
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/*tag= a
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                                                                                                                AATTTTAAGTGTAATTGGCTTATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAATAA
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                                                                                                                                                                                                                                                                                                                              TGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAA
                                                                                Gaps
                                                                                20;
            Sequence 2940 BP; 955 A; 514 C; 512 G; 959 T; 0 U; 0 Other;
                                           Score 124; DB 8; Length 29
Pred. No. 1.6e-13;
0; Mismatches 380; Indels
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nilarity 50.7%;
Conservative 0
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                                                                   Best Local Simi
Matches 412;
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SEQ ID #238.

Staphylococcus aureus contig

(first entry)

16-MAR-1999

AAV74549

exaxyxak

BP

AAV74549 standard; DNA; 3775

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of the invention. The DNA sequence are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM, Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of solvential and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
         Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AATTAAAATGCTTGTTGCTTTGCTTTCCTACTTGTTTTAGCAGGATGTAGTGGAA
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                                                                                                                                                                        /*tag= a //note= "these bases represent a line of missing text the sequence listing in the specification. They are included to maintain the nucleotide numbering given the specification for this DNA sequence"
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in the production of a
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Pred. No. 1.7e-13;
0; Mismatches 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from stored on computer readable medium and used
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                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
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Best Local Similarity 50.7%;
Matches 412; Conservative (
                                                                     toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                       *tag=
                                                                                                        Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                <u>ragaaargaaagriracgarcaarrarcaaacgacc</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAACAAAGCAAGTTCTAACGAACCTTCACTA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCAGATCCAAATGCGAAAGATGCTGCATTA
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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid (2) a host cell containing the vector; (3) an isolated cupleptide acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cell polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological companion acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the straint compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for the admitifying proteins or screening for homologous nucleic acids are useful for for diagrams or the proliferation of an organism. The antisense nucleic acids are useful for for diagrams and diagrams and diagrams and diagrams or for a diagram or for a diagram or for an expensive and diagrams or for a diagram or for an expensive and diagrams or for a diagram or for an expensive and diagrams. The antisense nucleic acids are useful for for a diagram or diagram or for an expensive or confidence or confidence or diagrams.
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                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
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                                                                                                                                                                                                                                            Haselbeck R,
Yamamoto R,
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Pred. No. 1.4
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Carr GJ,
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                               ELITRA PHARM INC.
                                                                                                                                                                                                                                            Zamudio C,
Trawick JD,
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
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                                                                                                 CAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTATTGCTGATAATAAT
                                                                                                                                                                                     <u> AGACACAAAGGTATTTATAAAGACTTAAATTAAAATTGCTCCTACGATTGAACTGAAAAGT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. epidermidis genomic polynucleotide sequence SEQ ID NO:3782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACAAAGCAAGTTCTAACGAACCTTCACTA
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                                       242 CAGTTATGTTTGATCCATCAACAAGCAATAACGATCACTTTGCTGAAATGACAGAAACAT 301
                                                                                                        302 TTAAACAAATTGCAAAAGCAGTTGGAAAAGAAGAAGAAGGTAAAAAAAGTATTAGCTGATA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a mutileic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
                                                                                 TTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAAACGCTTAGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 GGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTCTTGAGTATTCATTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 GATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAA
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CGAT-----TGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 861 BP; 348 A; 123 C; 158 G; 232 T; 0 U; 0 Other;
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10.9%; Score 110.2; DB 8;
Best Local Similarity 51.8%; Pred. No. 5.1e-11;
Matches 358; Conservative 0; Mismatches 313;
                                                                                                                                                                   542 ACGATAAGAAATTGAAGAATATAAAAAAGAAAT 575
                                                                                                                                                                                                         362 regaraaagcarregereargeaaaagcaaaaar 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 4579; 49pp; English.
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                                                                                                                                                                                                                                                                                                                     ВЪ
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                                                                                                                                                                                                                                                                                                                   ACF74610 standard; DNA; 861
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
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and (II), given in AGGB1454 to AAGB3120, from Staphylococcus epidermidis.

and (II) can have antibacterial activity and therefore can be used in vacadination. The nucleic acids (I) was be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) fand/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their creatment of S. epidermidis processed to assay for other inhibitors of their treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH55090 to AAH540 to AAH540 to AAH540 to AAH540 to AAH540 to AAH540 to AAH540 to AAH540 to AAH540 to 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAAAGAGTCATCAAA 119
                                                                        to AAH53970 represent nucleic acids (I) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 3046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3046 BP; 1103 A; 468 C; 436 G; 1039 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.9%; Score 109.4; DB 4
Best Local Similarity 95.0%; Pred. No. 7.7e-11;
Matches 113; Conservative 0; Mismatches 6
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Yamamoto R,
                       Claim 8; Page 1413-1414; 2188pp; English.
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Carr GJ,
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25-02T-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-036289P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for SEQ ID NO:4455 to 4464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacter cloacae.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        design; gene
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P-PSDB; ABU28130.
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
of uncleic acid; (2) a host cell containing the vector; (3) an isolated
contypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
contypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contiferation or the activity of a gene in an operon required for
proliferation or the activity of a gene in an operon required for
contiferation or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
contiferation or which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising strains in which the
compound's activity; (11) a culture comprising experiment of an organism. The antisense nucleic acids are useful for
contiferation of an organism. The antisense nucleic acids are useful for
contiferation are screening for homologous nucleic acids are useful for
contiferation are proliferation to isolate candidate molecules for rational 316 193 436 137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTGAGT 196 376 254 GAÁCGCGCGCGCAGCCGAGCCTGGAAGCCATTGCTGCCCTGAAACCAGACCTGATCATTG 313 AACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTTCAA 496 433 AAGCTTTAGGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTG 556 aagrogradgraaaaacgagagargcaggcgcgcrcrggaacaacaraaaagagaagargg 493 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 74 accaccaaccaccaccactracactrcarraaaccccacaaccaccacaaccacaac 194 Accangcada a confector con a defector con a confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector de confector CTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATTAAAATTGCTCCTACGATTG 197 ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA 134 TCTCGTTCGCCCGATGCGCTGGCCGCCGTGGACGTCAGCCCCGATCGGTATTGCCGACGATA 257 ACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAG GAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTATTG 374 ISCITIAAGICCCGCAACGAAACCIACGCIGAAAITIIGCACICAGCGGCIAICAICGGCG Gaps New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. ö Length 900; Sequence 900 BP; 198 A; 266 C; 256 G; 180 T; 0 U; 0 Other; Indels 10.2%; Score 103.2; DB 8; 52.9%; Pred. No. 9.7e-10; rative 0; Mismatches 198; NO 19870; 1766pp; Matches 222; Conservative Local Similarity SEQ ID Claim 14; 317 437 434 377 497 Query Match 셤 ò g g ò g 8 셤 8 8 8 셤 Š ઠે

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437 AACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAAACAATTTCAA 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid from Photorhabdus luminescens, useful for producing insecticidal polypeptides active against Lepidoptera, and for producing insect resistant transgenic plants.
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/product= "Photorhabdus luminescens insecticide protein
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P-PSDB; ADR20889, ADR20891.
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                                                                                                                                                                                                                                                                   Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.
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Locus ACF67367 Accession Acf67367
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The invention comprises the amino acid and coding sequences of proteins from Photorhabdus luminescens which are active against insects. The proteins of the invention are toxic to Lepidoptera, specifically the genera Plutella, Heliothis, Heliotoverpa, Spodoptera and Ostrinia. The DNA and protein sequences of the invention are useful in the preparation of transgenic, insect resistant plants, specifically wheat and maize. The present Photorhabdus luminescens genomic DNA contains the coding sequence for the two insecticide proteins of the invention.
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ilarity 51.6%; Pred. No. 1.8e-08;
Conservative 0; Mismatches 207; Indels 0;
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Continuation (9 of 13) of ACF65388 from base 800001 (Photorhabdus luminescens nucleotide WP Sequence split into 13 fragments LOCUS ACF65388 Accession Acf65388
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Pred. No. 1.9e-08;
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Best Local Similarity 51.6%;
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OM nucleic - nucleic search, using sw model

August 26, 2005, 03:38:21; Search time 3906 Seconds (without alignments) 9823.037 Million cell updates/sec Run on:

US-10-724-972A-2580 1008

1 ggagtggaatcagtgagagg.....gtaaaaaagataataagtaa 1008 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched: 68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description			CG757757 P053-1-D0	CL082569 CH216-167	AL226115 Tetraodon		BH651171 BOMJP20TR	CR734084 Tetraodon	AG429915 Mus muscu	CL461494 SAIL_1148			~	AL073856 Drosophil	AG386893 Mus muscu	CL078552 CH216-151	_	_	CL119201 ISB1-76J1	CL694436 PRI0164b_	CG755650 P051-1-G0	AG332167 Mus muscu	AL229763 Tetraodon	AL108642 Drosophil
	, di	CL674627	CF307287	CG757757	CL082569	CNS033GQ	CNS0021J	BH651171	CR734084	AG429915	CL461494	CL101048	CF238805	CL038406	CNS00HX9	AG386893	CL078552	AG278469	CG745927	CL119201	CL694436	CG755650	AG332167	CNS036A2	CNS017Y0
	Query Match Length DB	801 9	625 7	1566 9	1632 9	1135 9	1101 9	773 8	1172 3	1362 9	1042 9	1017 9	1626 7	1594 9	1101 9	1519 9	1402 9	1506 9	1225 9	1256 9	776 9	1231 9	1251 9	625 9	1101 9
de	Query Match	9.6	9.4	8.7	8.7	8.6	8.6	8.3	8.3	8.2	8.1	8.1	8.1	8.1	8.0	8.0	8.0	8.0	8.0	7.9	7.9	7.9	7.9	7.9	7.9
	Score	96.8	95.2	87.4	87.4	96.6	86.4	83.6	83.6	82.4	81.6	81.4	81.4	81.2	80.8	80.8	80.6	80.4	80.2	80	79.6	79.6	79.6	79.2	79.2
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_	-	CL078538 CH216-151	CL077122 CH216-143	BF273407 GA ED001	CL078190 CH216-148	CG754010 P049-2-C0	_	_	CG753732 P048-4-G0	CL081338 CH216-161	-	CG744815 P037-3-B0	CL110653 ISB1-53P2	CD388253 AGENCOURT	CL037168 CH216-42N	AG288477 Mus muscu	CG750869 P045-2-E1	AJS91978 Arabidops	CV481731 AGENCOURT	AL441457 T7 end of	
CG744812	CG757503	CL078538	CL077122	BF273407	CL078190	CG754010	AG350118	CC268594	CG753732	CL081338	CG758143	CG744815	CL110653	CD388253	CL037168	AG288477	CG750869	AJ591978	CV481731	CNS07E8R	
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79.2	79	79	78.8	78.8	78.8	78.8	78.8	78.6	78.6	78.4	78.4	78.4	78.4	78.2	78.2	78.2	78.2	78.2	78	78	
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ALIGNMENTS

RESULT 1 CL674627 LOCUS DBFINITION	CL674627 PRIO112c G03 2 - PRIO112c.BR (801) Mixed stage fosmid library of P. PRIO112c GO3 2 - PRIO112c.BR (1901) Mixed stage fosmid library of P. PRIO112c Ampence.
z	462
KEYWORDS SOURCE ORGANISM	GSS. Pristionchus pacificus Pristionchus pacificus Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
REFERENCE AUTHORS TITLE	T (bases 1 to 801) Srinivaean, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. Appabb: an Accedb database for the nematode satellite organism Pristionchus pacificus
JOURNAL	Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany
	Tel: 00497071601371 Fax: 00497071601498 Fax: 00497071601498 Fax: 00497071601498 This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: Fosmid ends.
FEATURES BOULCE	<pre>Location/Qualifiers 1. 801 / organism="Pristionchus pacificus" /orfanism="California" /db_xref="taxon: 54126" /db_xref="taxon: 54126" /clone lib="Mixed stage fosmid library of P. pacificus var. California" /crea="Worter: Progrid Perfor"</pre>
ORIGIN	
Query Match Best Local Sim Matches 218;	Ouery Match 9.6%; Score 96.8; DB 9; Length 801; Best Local Similarity 51.9%; Pred. No. 3.3e-09; Matches 218; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

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Gaps

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Mismatches 203; Indels

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Conservative
217;
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Bukaryota, (japonica cultivar-group)

Bukaryota, (japonica cultivar-group)

Bukaryota, (japonica cultivar-group)

Bukaryota, (japonica cultivar-group)

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Bukaryota, (japonica cultivar-group)

Bukartoideae; Oryzeae, Oryzeae; Dijopsida; Poales; Poaceae;

Bukartoideae; Oryzeae, Oryzeae, Oryzeae; Divara.

Bukartoideae; Oryzeae, Oryzeae, Oryzeae; Divara.

Buxim, J.S., Juu, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-grane State Squenching Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomica and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongIn, Kyeonggi, Korea

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Fax: 82 31 320 6193

Buail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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CF307287

HDA1--06-E11.gl OBHDAC1-overschessing transgenic rice lambda phage CDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA clone HDA1--06-E11, mRNA sequence.
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/clone="HDA1--06-E11"
/tlssue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="Ecoli SOLR"
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phage CDN library I (HDA1)"
                                    ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA
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mol type="mRNA"
cultivar="Nackdong"
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Score 95.2; DB 7; Length 625; Pred. No. 6.9e-09;

9.4%;

Query Match Best Local Similarity

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1 (bases 1 to 1566)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Butrjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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  137 AGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGAGT
                                                      615 AGGACGAACACGCACGTTTACACTCGAAAAACGCCACAACGGATTGTGGTGCTGGAAC
                                                                                                             197 ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATA
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/clone_llb="#ppa Ecost BAC Library"
/note="frhe library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Pred. No. 2.6e-07;
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Class: BAC ends.
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/mol_type="genomic DNA"
/strain="California"
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Best Local Similarity
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Contact: Richard K Wilson
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Similarity 45.3%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                  614 CTGCTAAATCAGGTTTGCTTGTTCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC
                     254 ATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
                                           314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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/organism="Xenopus tropicalis"
/orl type="genomic DNA"
/strain="Nigerian frog"
/db xref="texon:8364"
/clone="CH216-16795"
Contact: Kitumical Center
Menington University School of Medicine
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
                                                                           Insert Length: 175000 Std Error:
Seg primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                 High quality sequence start: 1062
High quality sequence stop: 1114.
Location/Qualifiers
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and mamnoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPRC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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TIGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAAATAAAATTGCTCCTACGA
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Rerygota;
Byeoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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/note="Genoscope sequence ID : COAG208DH12SPl~end
PUC-Ori"
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="208P24"
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46.0%; Pred. No. 3.8e-07;
tive 9; Mismatches 330;
                                                974 TATCTAAGAAAGATAGTAAAAAAGATAATAAGTAA 1008
                                                                                                 Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                      1135 bp
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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                                                                                                Brassica oleracea
Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATTTTGATGCTTTTAAAACAATTT 493
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                                                                                                                                                                                                        Town.C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
BOMJP20TR BO 2 3 KB Brassica oleracea genomic clone BOMJP20,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BOMJP20"
/clone lib="BQ_2 3 KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
                                                                                                                                                                                                                                                                                                                                                                                                haploid provided by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Score 83.6; DB 8;
51.0%; Pred. No. 1.5e-06;
ive 0; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                     Rockville,
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/strain="TO1000DH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Tel: 301-838-3523
Fax: 301-838-0208
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                                                             BH651171.1 GI:18709113
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  is from a doubled b
  primer: TR
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Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                    TTTTTTTTTTTTTNAAAANAWKAAATNATAATTTTTAATTTTAAAKAAKWDTAAATAA 125
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          1. .1101
/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROSN11"
/clone lib=RPCI 98"
/note="end : TET3"
                                                                                                                                                                                                                         44; Mismatches 447;
                                                                                                                                                                                    8.6%; Score 86.4; DB 9; 39.7%; Pred. No. 4.1e-07;
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HTC 19-AUG-2004 linear CR734084 1172 bp mRNA Tetraodon nigroviridis full-length cDNA. CR734084 LOCUS DEFINITION ACCESSION CR734084/c

GSS 19-FEB-2002

linear

DNA

ď 773

RESULT 7 BH651171/c LOCUS

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/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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BAC end Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:57486"
/clone="MSMg01-304L12.TJ"
                         171
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                  865 AAATTAAACGCTGTGAAAAATCAA
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                                                                                                                                                                   Mus musculus molossinus
Mus musculus molossinus
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: EcoRI
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                                                                                                        Mus musculus
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LIBRARY
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GSS.
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R.Site 2
                                                                                        AG429915
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                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTAAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAATCG
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                                                                                                                                                                                                                                                                                                                          8.3%; Score 83.6; DB 3; Length 1172; 47.2%; Pred. No. 1.5e-06; ive 0; Mismatches 354; Indels 7;
            HTC; cDNA; full-length; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                               /organism="Tetraodon nigroviridis"
|mol_type="mRNA"
|db_xref="taxon:99883"
                                                                                                                                                                                                         http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        tissue_type="fish"
 GI:51232422
                                                                                                                                                                                                                                                                                                                                         Similarity 47.2
23; Conservative
                                                                                                                                Submission
                                                                                                                   Genoscope
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2 (bases 1 to 1362)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN) Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorieger.iken.jp), URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadal, Tsukuba 135-0074 Japan e-mail: abe@rtc.riken.jp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 2.6e-06;
0; Mismatches 480; Indele
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CL101048 1017 bp DNA linear GSS 05-JAN-2004 ISB1-3604 Sp6.1 ISB1 Kenopus tropicalis genomic clone ISB1-3604, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                              254 ATAACAAAAAAAATCGTATTAAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACACGATAAGAAAA 553
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.

( (Dases 1 to 1017)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
                                                              /db.crypc=_corm.crypc=_
/db.cref="sAIL 1148 D03 v1"
/clone="sAIL 1148 D03 v1"
/clone lib="sAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                             TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAAACAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                TAGGAACACGTAAGCAACCTAAGAAGAAATCAGTAAACTTAAATTA
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                                                                                                                                                                                                                                    Query Match 8.1%; Score 81.6; DB 9;
Best Local Similarity 54.1%; Pred. No. 3.8e-06;
Matches 185; Conservative 0; Mismatches 153;
'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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/mol_type="genomic DNA"
/db_xef="texaon:8364"
/clone="ISB1-3604"
/clone="ISB1-3604"
                      /mol_type="genomic DNA"
/ecotype="Columbia"
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High quality sequence stop: 136.
Location/Qualifiers
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ABRC Stock Number CS642250; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Bloological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAIL_1148_D03.v1 SAIL Collection Arabidopsis thaliana genomic clone SAIL_1148_D03.v1, genomic survey sequence.
                                                                           Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Core eudicots; Core eucosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(Bases 1 to 1042)
Sessions, A., Burke, B., Presting, G., Aux, G., McElver, J., Patton, D., Bertich, B., Ho, P., Bacweden, J., Ko, C., Clarke, J.D., Cotton, D., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system
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                                                                                                                                                                     617 CTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAAC 676
                                                                                                                                                                                                                                                                                                                                                                 TAATGACAAACAAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCCTG 856
                                                                                                                                                                                                                                                                    TATGGAAGAAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGACTTAT
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Arabidopsis thaliana
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Location/Qualifiers
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3054 Cornwallia DA
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Applied Trait Genetics
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE PUBMED COMMENT

FEATURES

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1594 bp DNA linear GSS 31-DEC-2003 CH216-46A6 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-46A6, genomic survey sequence.
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/clone_lib="NICHD XGC_Emb6"
/note="Vector: pGWV-SPORT6.1, Site 1: NotI; Site_2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
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                                                                                                                                                                                                                                                                                                                   GAACTGAAAAGTTTCGATGGAGATTATAATGAAAAT---ATTGATGCTTTTAAAACAATT
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                                                                                                                                                                              Gaps
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                                                                                                                                          Length 1626;
                                                                                                                                        Score 81.4; DB 7; Length 1
Pred. No. 4.2e-06;
0; Mismatches 413; Indels
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I basea 1 to 1626)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
       BAC
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AGENCOURT 15099447 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone
IMAGE:6995950 5', mRNA sequence.
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheada, WD 20892
Email: egapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clond through the I.M.A.G.E. Consortium/LLNL at:
thtp://image.llnl.gov
Plate: LLAM14680 row: g column: 21
High quality sequence start: 71
High quality sequence start: 71
High quality sequence start: 71
                                                                                                                                             254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
                                                                                                                                                                          314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGATTTAATTA
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       /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"
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                                                                         8.1%; Score 81.4; DB 9; Length 1017; 54.2%; Pred. No. 4.1e-06;
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/tissue_type="neurula"
/dev_stage="embryo, stages 14-19"
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Xenopus tropicalis
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'db xref="taxon:8364"
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                                                                                                           Conservative
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Matches 188;
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CF238805
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1405

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Obtermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruiffly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecorganic strain of Drosophila DNA provided by the BDGP from the isogenic strain of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                             1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR35W04 of RPCI-98 library from Drosophila melanogaster (fruit Lly), genomic survey sequence.
                                                                                                                                 292 AAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGT 351
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                                                                                         854 CTGTATGGAAGAAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGACT
                                                                                                                                                                                914 TATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAAT
  794 TCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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44.7%; Pred. No. 5.5e-06;
ive 31; Mismatches 178; Indels
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/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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Best Local Similarity 44.7%
Matches 169; Conservative
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Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Enharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batracotia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1594)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 TIGAAGAATATAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATIGCCTGCAGTAG
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Pred. No. 4.6e-06;
0; Mismatches 423; Indels 0;
                                                                                                                                                                                                                             Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 471
High quality sequence stop: 522.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-46A6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.0%;
Matches 332; Conservative
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              SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegescrikken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:s1-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadal, Tankuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                            AG386893 1519 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-201E07.TJ, genomic survey
                               471
                                                                                                                            ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGAAGAAAAAAAGCC 531
                                                                                                                                                      209 Адасаттитдаадададамдимдадасттидамдадададададамитдададссс 150
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                   AAACTTAAACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGAC
                                                                     TTAAATTAAAATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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/clone_lib="MSMg01 Mouse Male BAC Library"
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mol_type="genomic DNA"
sub_species="molossinus"
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Pred. No. 5.5e-06;
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clone="MSMg01-201E07.TJ"
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Location/Qualifiers
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Mus musculus molossinus
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: EcoRI
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Best Local Similarity
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AG386893/c
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1402 bp DNA linear GSS 31-DEC-2003
CH216-151D21_SpS.1 CH216 Xenopus tropicalis genomic clone
CH216-151D21, genomic survey sequence.
CL078552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       734 AAGGACCTTACTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT 793
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(bases 1 to 1402)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mandis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
                                                                            434 TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
                                                                                                                                                                                                                                                                                                                                                                                                 CTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC
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                                                                                                                 314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACTTAAATTA
                                                                                                                                                                                               494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
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Xenopus tropicalis
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JOURNAL
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2 (bases 1 to 1506)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                and Chemical Research (IKERN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattoriegec.riken.jp), URL:http://hgp.gsc.riken.go.jp/, Trel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadal, Tsukuba, 305-0074 Japan phone: 81-288-36-9189, fax: 81-298-36-9199
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                              Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.4; DB 9; Length 1
Pred. No. 6.7e-06;
0; Mismatches 331; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-048M18.T7'
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 musculus molossinus
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Local Similarity 46.6%;
nes 290; Conservative
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Mus musculus molossinus DNA, clone:MSMg01-048M18.T7, genomic survey
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                                                                                                                                                                                                                                                                                          /cell line="Stock 248 F7A2, inbred N7"
/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
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                Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
High quality sequence start: 867
High quality sequence stop: 918.
Location/Qualifiers
                                                                                                                                                                                       /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="CH216-151D21"
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Contact: Richard K Wilson
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Mus musculus molossinus
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AG278469.1
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CL119201 1256 bp DNA linear GSS 05-JAN-2004 ISB1-76J12 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-76J12, genomic survey sequence.
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                                                            494 CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
                                                                                                  614 CTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases I to 1256)
Mcremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
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    1.256
    /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db xref="texon:8364"
/clone="ISB1-76J12"

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High quality sequence stop: 402.
Location/Qualifiers
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Neodiplogasteridae; Pristionchus.
1 (Dases I to 1225)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                              731 TTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTA 790
                                                                                                                                                                             /db xref="taxxon:54126" /db xref="taxxon:54126" /clone_lib="Ppa EcoRI BAC Library" /note="The library was generated by a partial digest of the genemic DNA with EcoRI and cloning into the BAC vector."
    791 TGTTCATAATGACAAACCAAGCTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAG
                                                                                                    254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
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Max-Planck Institute for Developmental Biology
Maya-planck Institute for T2076, Germany
Tel: 00497071601371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ralf.sommer@tuebingen.mpg.de
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/strain="California"
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Best Local Similarity 41.99
Matches 316; Conservative
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Sommer, R.J.

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POSI-1-G09.yc Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Hodiplogasteridae; Pristionchus.
1 (bases 1 to 1231)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
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         Neodiplogasteridae; Pristionchus.

1 (bases 1 to 776)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J Appabls an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                                                                                                                                                                                                                                                                                                                                                                                Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 79.6; DB 9; Length 7
Pred. No. 9.4e-06;
0; Mismatches 174; Indels
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/clone lib="Mixed stage fosmid library
var. California"
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                                                                                                                                                                                                                                                   Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
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                                              BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
                                                                                                                                                                                                                               Gaps
             /clone lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"
                                                                                                                                                                                                                               .;
0
                                                                                                                                                                 Score 80; DB 9; Length 1256;
Pred. No. 8e-06;
0; Mismatches 474; Indels
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Pristionchus pacificus
                                                                                                                                                                    tch 7.9%;
al Similarity 37.2%;
281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  survey sequence.
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P. pacificus

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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chour, Tsurumi. Ku. Yokohama, Kanagawa 230-0045, Japan 1-22 Suehiro-chour, Tsurumi. Ku. Yokohama, Kanagawa 230-0045, Japan Tel. 81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMG01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-288-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG332167 1251 bp DNA linear GSS 02-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-122E04.T7, genomic survey
                            914 TATGGGCAAGATCACGTGGTTTAATFTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAAT 973
                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                Kojima, T. and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mixture of kidney and spleen
/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                              974 TATCTAAGAAAGATAGTAAAAAAGATAATAAGTAA 1008
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Pred. No. 9.6e-06;
0; Mismatches 168;
                                                                                          Hattori,M., Toyoda,A., Noguchi,H., 1
BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MSMg01-122E04.T7"
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1. .1251
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ilarity 51.0%;
Conservative
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 79.6; DB 9; Length 1231; 41.1%; Pred. No. 9.6e-06; ive 0; Mismatches 445; Indels 0.
                                                                             Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannatr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
                                  Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                        pacificus"
                                                                                                                                                                           Bmail: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                        organism="Pristionchus
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                                                                                                                                                                                               Class: BAC ends.
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                                                                                                                                                                                                                                                                              625 bp DNA linear GSS 01-SEP-2000 genome survey sequence PUC-Ori end of clone om Tetraodon nigroviridis, genomic survey
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
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Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                     434 ITGAACTGAAAAGTTTCGATGAAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT 493
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/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:99883"
/clone="215D13"
/clone lib="G"
/note="Genoscope sequence ID : COAG215CB088P1~end
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Pred. No. 1.1e-05;
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215D15 of library G fro
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AL229763.1 GI:7888758
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Similarity 48.2%;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.wt - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Ettude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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300 AAAATACACTICTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAA
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha;
Ebyydroidea, Drosophilidae, Drosophila.
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/mol type="genomic DNA"
/db_Xref="taxon:1227"
/clone="BACN37H18"
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/plasmīd="pBeloBAC11"
/note="end : T7"
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Srinhivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Srinhivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Snintegrated physical and genetic map of the nematode Pristionchus
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Max-Planck-Institute for Developmental Biology
Speannatr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Neodiplogasteridae; Pristionchus.
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Fax: 00497071601498
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Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                    GAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTA 358
                                                                                                        AACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATA 418
                                                                                                                                          AAATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATG 478
                                                                                                                                                                                                 479 CTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGAAGGTAAAAAACGCTTAGAAG 538
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Neodiplogasteridae, Pristionchus.
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40.2%; Pred. No. 1.2e-05;
ive 0; Mismatches 455; Indels
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'strain="California"
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Matches 306, Conservative
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                                                                                /db_xref="taxon:54126"
/db_xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
                                                                                                                                                                                                                                                      254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
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                                                                                                                                                                                            Score 79; DB 9; Length 1392;
Pred. No. 1.3e-05;
0; Mismatches 412; Indels ·
                                                     /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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ralf.sommer@tuebingen.mpg.de
BAC ends.
                       Location/Qualifiers
1. .1392
                                                                                                                                                                                               tch 7.8%;
al Similarity 44.9%;
338; Conservative
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Best Local Similarity
 Email:
Class:
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RESULT 27 CL078538

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CL077122 1162 bp DNA linear GSS 31-DEC-2003 CH216-143E5 Sp6.1 CH216 Kenopus tropicalis genomic clone CH216-143E5, genomic survey sequence.
1536 bp DNA linear GSS 31-DEC-2003
CH216-151C11_Sp5.1 CH216 Xenopus tropicalis genomic clone
CH216-151C11, genomic survey sequence.
CL078538
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                                                                                                                                                                                                         Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopous; Silurana.

Xenopodinae; Xenopus; Silurana.

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

Maphysical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell line="Stock 248 F7A2, inbred N7"
/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
High quality sequence start: 1061
High quality sequence stop: 1145.
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Similarity 51.3%; Pred. No. 1.3e-05;
78; Conservative 0; Mismatches 169;
                                                                                                                                                                     Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
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                                                                                                                             CL078538.1 GI:40534451
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Bukaryota, Viridipantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridipantae; Streptophyta; Core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases I to 1188)
1 (bases I to 1188)
1 (hases I to 1188)
1 (hases I to 1188)
1 (hases I to 1189)
1 integrated nalysis of the genetics, development, and evolution of the cotton fiber
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/sultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Eb0017023f"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                  794 TCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 ATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG
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/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
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larity 39.5%; Pred. No. 1.4e-05;
Conservative 0; Mismatches 384;
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Clemson University
100 Oordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288

    .1185
/organism="Gossypium arboreum"
/mol_type="mRNA"

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Seq primer: TAATACGACTACACTATAGGG
High quality sequence start: 540
High quality sequence stop: 1175.
Location/Qualifiers
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                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                                                                                                                                                                                         X remitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, Y., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, Y., McContact map of the xenopus tropicalis genome topublished (2003)

Contact: Richard K Wilson Genome Sequencing Center Washington University Showled on Washington University Showled Center Washington University Showled Sequence Sequence State: 7570

Insert Length: 175000 Std Brror: 0.00

Seq primmer: Sp6 ATTAGGTGACACTATAG

Class: BAC ends

High quality sequence state: 757

High quality sequence stop: 808.
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7.8%; Score 78.8; DB 9; Length 1162;
Best Local Similarity 45.5%; Pred. No. 1.4e-05;
Matches 316; Conservative 0; Mismatches 378; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus tropicalis"
mol_type="genomic DNA"
ferrain="Nigerian frog"
db_xref="texon:8364"
clone="CH216-143E5"
                                                                      Xenopus tropicalis (western clawed frog)
                         GI:40533035
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Query Match 7.8%
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En (bases I to 1217)

S Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

A Dupublished (2003)

Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 229
High quality sequence stop: 312.
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             434 TTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATTT
                                                              CAAAAGCTTTAGGTAAAGAAGAAGGAAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAA
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Xenopus tropicalis
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/mol_type="genomic DNA"
/strain="Nigerian frog"
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/clone="CH216-148G2"
sex="male"
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UG/D4010 1276 bp DNA linear GSS 24-OCT-2003 P049-2-C03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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Pristionchus pacificus
Eukaryota; Metazca; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                           Indels
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Pred. No. 1.4e-05;
0; Mismatches 412;
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL.http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170; Uhpg.gsc.riken.go.jp/, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, Trankuba institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone; 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                   AG350118 1472 bp DNA linear GSS 02-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTG 313
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             914 TATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGAAT 973
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 1.4e-05;
0; Mismatches 456; Indels
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/organism="Mus musculus molossinus"
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BAC end Sequences of Library MSMg01
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/sub_species="molossinus"
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               Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J. An integrated physical and genetic map of the nematode Pristionchus
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/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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                                                                                                                                         Contact: Sommer RJ
Evolutionary Biology
Max-Plantck-Institute for Developmental Biology
Spannustr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                        Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                           pacificus"
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Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                         organism="Pristionchus
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'strain="California"
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Matches 305; Conservative
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1 (Bases 1 to 1352)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                             614 CTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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CH261-67F12_Sp6.1 CH261 Gallus g
genomic survey sequence.
CC268544
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High quality sequence start: 19
High quality sequence stop: 132.
Location/Qualifiers
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CC268594.1 GI:30619779
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                                                                           /sex="female" /cell_line="UCD001, inbred 256" /cell_line="UCD001, inbred 256" /clone_lib="CH261" /nclone_lib="CH261" /nclone="Vector: pTARBAC2.1; Site_l: EcoRI; Site_l: EcoRICH261 Female Chicken library - for library and clone ordering information: http://www.chori.org/bacpac"
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.larity 40.5%; Pred. No. 1.5e-05;
Conservative 0; Mismatches 449;
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-67F12"
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Pristionchus pacificus
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Bukaryotasereridae, Nematodae, Chromadorea, Diplogasterida,
Bucadiplogasteridae, Pristionchus.

1 (bases 1 to 1811)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
CG753732 1811 bp DNA linear GSS 24-OCT-2003 P048-4-G03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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                                                                                                                                                                                                                                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
et an 10497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                         4ol. Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="California"
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                                                               CG753732.1 GI:37978509
                                                                                                                                                                                                                                                                                         Contact: Sommer RJ
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                                                                                                                                                                                                                                                               AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGGCGTATGT 793
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library.
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A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL081338 1163 bp DNA linear GSS 3
CH216-161H3 RM4.1 CH216 Xenopus tropicalis genomic clone
CH216-161H3, genomic survey sequence.
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Best Local Similarity 44.0%; Pred. No. 1.7e-05;
Matches 331; Conservative 0; Mismatches 422; Indels
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Washington University School of Medicine
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Insert Length: 175000 Std Error: 0.00
Seq primer: RM4 ctcaagggcatcggtcgagc
Class: BAC ends
High quality sequence start: 826
High quality sequence stop: 926.
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/strain="Nigerian frog"
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/clone="CH216-161H3"
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                                         1. .1297
/organism="Pristionchus pacificus"
/ordanism="Pristionchus pacificus"
/ordarain="california"
/db_xxef="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tas: 00497071601371
Fax: 00497071601498
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Neodiplogasteridae; Pristionchus.
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genomic survey sequence.
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AUTHORS
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CL110653/c
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CG744815
1380 bp DNA linear GSS 24-OCT-2003
P037-3-B04.za Ppa BCORI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
CG744815.1 GI:37965683
                                                                                                                                               1 (bases 1 to 1380)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                614 CTGCTAAATCAGGTTTGCTTGCTCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTC 673
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
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                                                                                                                     Chromadorea; Diplogasterida;
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40.4%; Pred. No. 1.7e-05;
iive 0; Mismatches 378; Indels 0
                                                                                                                                                                                                                                                                                Evolutionary Biology
Max-Planck-Innetitute for Developmental Biology
Max-planck: 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                  Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                        Email: ralf.sommer@tuebingen.mpg.de
                                                                                      Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazca; Nematoda; Chro
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                              mol type="genomic DNA"
strain="California"
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .1380
                                                                                                                                                                                                                                                                                                                                           00497071601498
                                                                                                                                                                                                                                                                    Contact: Sommer RJ
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Matches 256;
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AUTHORS
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1373
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                                                                                                          853
AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT 793
                                                                                                                                                                 Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (bases i to 1594)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ISB1-53P23"
/clone lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
                                                    794 TCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ATGATAACAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1594;
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46.2%; Pred. No. 1.7e-05;
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Mashington University School of Medicine
Email: submissions@wateson.wusfl.edu
Insert Length: 75000 Std Brror: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                        854 CTGTATGGAAGAATTAAACGCTGTGAAAAATCA 887
                                                                                                                                                                                                                                                                         1. .1594
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
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CL037168 11.0 bp DNA linear GSS 31-DEC-2003 CH216-42N18 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-42N18, genomic survey sequence.
                                                                                                                                                                                         TTAAATAAAATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAAT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Acnopodinae; Xenopus; Silurana.

1 (bases 1 to 1110)

Kremitzki, C., Carter J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
(2003)
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                                                                                                                                                  232 AAACCTGTTGGGATAGCGGATGATAACAAAAAAATCGTATTAATAAACCATTAAGAGAT
                                                                                                                                                                                                                                       292 AAAATTGGAAAATACACTTCTGTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGT
                                                                                                                                                                                                                                                                                                                                 AAACTTAAACCAGATTTAATTATTGCTGATAATAAACACACAAAGGTATTTATAAAGAC
                                                             CCTAAACGTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTT
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/clone_lib="CH216"
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Washington University School of Medicine
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Xenopus tropicalis
Pred. No. 1.8e-05;
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/mol type="genomic DNA"
/strain="Nigerian frog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 14
High quality sequence stop: 150.
Location/Qualifiers
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/clone="CH216-42N18"
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CL037168.1 GI:40491901
  Best Local Similarity 42.1%;
Matches 179; Conservative
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CL037168/c
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JOURNAL
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AGENCOURT_14304648 NIH_MGC_173 Homo sapiens CDNA 5', mRNA sequence.
CD388253
  /tissue_type="embryonic trophoblasts, made from WA01 stem
                                                                                                                                                         670
                                                                    610
                                                                                                                                                                                                                                                791 IGITCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                               L (Dases 1 to 2) 11.

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upubblished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDKW80 row: j column: 22
High quality sequence start: 16
High quality sequence start: 16
High quality sequence stop: 510.
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1 (bases 1 to 971)
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5D - full-length enriched;
                                                                                                                                                                                                                                                                                                                                     731 TTAAAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTA
                                                                    AAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAG
                                                                                                                                                            TAGCTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAA
                                                                                                                                                                                                                                                                                              7.8%; Score 78.2; DB 6; Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    851 ATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_173"
/note="Vector: pDONR201; Site_1:
LIBR_PRIMING - oligo_dr; METHÖD
LIBR_PROVIDER - Bradfield"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD388253.1 GI:31226341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 39 CD388253

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TITLE JOURNAL COMMENT REFERENCE AUTHORS

Query Match

ORIGIN

source

FEATURES

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                                                                                                                                                   240 TGGGATAGCGGATGATAACAAAAAAATCGTATTATAAACCATTAAGAGATAAAATTGG 299
                                                                                                                                                                                                                                                300 AAAATACACTTCTGTAGGAACACGTAAGCAACCTAAACTTAGAAGAAATCAGTAAACTTAA 359
                                                                                                                                                                                                                                                                                                         360 ACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATAA 419
                                                                                                                                                                                                                                                                                                                                   420 AATTGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATGC 479
                                                                                                                                                                                                                                                                                                                                                                                                                              480 TTTTAAAACAATTTCAAAAGCTTTAGGTAAAGAAGAAGGTAAAAAACCGCTTAGAAGA 539
                                                                                                                                                                                                                  /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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                                                                                              ;
                                                             Query Match

7.8%; Score 78.2; DB 9; Length 1110;
Best Local Similarity 48.7%; Pred. No. 1.8e-05;
Matches 203; Conservative 0; Mismatches 214; Indels 0;
                                  ORIGIN
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Search completed: August 26, 2005, 06:59:20 Job time : 3914 secs

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- nucleic search, using sw model OM nucleic August 26, 2005, 05:54:23; Search time 2119 Seconds (without alignments) 3112.522 Million cell updates/sec Run on:

US-10-724-972A-2580 1008 Perfect score:

1 ggagtggaatcagtgagagg......gtaaaaaagataataagtaa 1008

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Sequence:

7331713 seqs, 3271544945 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications Nat.

(gnn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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(gnn2_6/p Published Applications NA:*

/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
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Result		Query				
No.	Score		Match Length DB ID	DB	ID	Description
	1008	•	!	22	US-10-724-972A-2580	Sequence 2580, Ap
	993	98.5	993	17	17 US-10-282-122A-34954	Sequence 34954, A
'n	567	56.2		17	US-10-282-122A-7644	Sequence 7644, Ap
4	564.4			6	US-09-815-242-8156	Sequence 8156, Ap
ស	531.8			σ	US-09-815-242-4404	Sequence 4404, Ap
9	309.8	30.7		17	US-10-282-122A-35107	Sequence 35107, A
7	265.6			σ	US-09-815-242-8024	Sequence 8024, Ap

	264.6	26.2	957	σ	US-09-815-242-4194	Sequence 4194, Ap
	1 (1)	26.1	957	12	0-470-048B	a 301
-	0 263.2	26.1	960	17	0-282-122A-7	e 794
-		22.1	668	œ	US-08-781-986A-355	55,
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H		16.1	242	8	US-08-781-986A-2556	556
H		16.1	242	18	US-10-329-624-2556	
H		15.5	897	11	US-10-282-122A-30706	
Н		14.8	801	6		Sequence 2066, Ap
-	-	14.2	972	11	US-10-282-122A-9415	Sequence 9415, Ap
-			321	6	US-09-815-242-2107	107
0			321	17	US-10-282-122A-4605	
7	12		2115	8	US-08-781-986A-604	40
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7		12.3	066	21	US-10-470-048B-318	
7	3 124		666	16	US-10-278-946-15	
7			666	7	5-10-967-189-1	
7			3775	8	US-08-781-986A-238	238,
7			3775	18	US-10-329-624-238	
0	11		196	11	US-10-282-122A-10009	Sequence 10009, A
7	103	10.2	006	17	US-10-282-122A-19870	e 19870
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m		7	963	17	US-10-282-122A-17083	
n	78		1026	17	US-10-282-122A-32601	Sequence 32601, A
n o		7.7	431	σ	US-09-960-352-5558	Sequence 5558, Ap
М	77	7.7	478	19	US-10-021-323-6774	6774
٣		7.5	891	17	US-10-282-122A-33236	
m		7.5	1121	20	0-425-115-11570	Sequence 115706,
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Ω 4	5 72.6	7.2	446	σ	US-09-960-352-3400	Sequence 3400, Ap

ALIGNMENTS

RESULT 1 US-10-724-972A-2580 ; Sequence 2580, Application US/10724972A ; Department of US-10-734A1 ; General information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information infor
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES KELATING TO STAFFILLOCUCIOS ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: PATHO3-16
; CURRENT APPLICATION NUMBER: US/10/724,972A ; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969 ; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001 ; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964 ; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779 ; PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 2580 ; LENGTH: 1008 ; TVPE: DAA
, ORGANISM: S.epidermidis US-10-724-972A-2580

ö Gaps ö Length 1008; Indels 100.0%; Score 1008; DB 22; 100.0%; Pred. No. 3.1e-162; iive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 1008; Conservative

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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yorant
APPLICANT: Yorant
APPLICANT: Yorant
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT PAPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,846
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-05-66
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PRIOR FILING DATE: 2000-05-66
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PRIOR FILING DATE: 2000-10-20-66
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-10-20-66
PRIOR APPLICATION NUMBER: 60/269,308
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98.5%; Score 993; DB 17; L
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 993; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Staphylococcus epidermidis US-10-282-122A-34954
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyakind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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                                                                                                                     61 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCCAAGTAAAGAGTCATCAAAA 120
       TIGCCIGCAGTAGCTGCTAAATCAGTTTGCTTCATCCAAGCAACTCTTATGTTGGT
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US-10-282-122A-34954 ; Sequence 34954, Application US/10282122A

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56.2%; Score 567; DB 17; Length 9

Best Local Similarity 73.6%; Pred. No. 3.9e-87;

Matches 723; Conservative 0; Mismatches 260; Indels
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-29

PRIOR FILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

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APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Garn
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yau, H.
APPLICANT: Yau, H.
APPLICANT: BOTSYth, R.
APPLICANT: BOTSYth, R.
APPLICANT: BOTSYTH, R.
APPLICANT: APPLICATION NUMBER: 60/201,078
REIOR FILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR PRILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                  481 TCAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACGATAAGAAA
                                                                ATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAAACAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-10-282-122A-7644
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GGAACGATGAGAGGTCTAAAAACTTTTTAGTATTTGGGATTAATAGTTGCCTTATTTTA
                                                                                       ACTICIGIAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACCAGAT
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                                                                                                                                    GITGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAAACACCCTAAAACGTGTTGTT
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US-09-815-242-4404
; Sequence 4404, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
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  AAGGACCTTACTTACAAATGAACACTGAAACTTTATCTCAAGTGAATCCTGAGCGTATGT
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APPLICANT: Obleson, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE ELITRA.011A
FILE REFERENCE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/205, 625
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25, 625
PRIOR FILING DATE: 2000-11-27
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Staphylococcus aureus
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US-09-815-242-8156
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US-09-815-242-8156
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA,034A
CURRENT FILING DATE: 2003-02-20
RIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
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                                                       541 AGAAATCAAAAAGTGCTTCCAGCAGTTGTTGCTAAAGCTGGTTTATTAGCACATCCAAAC
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: Zamudio, Carlos

: Malone, Cheryl

: Haselbeck, Robert

: Ohlsen, Kari

: Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
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Trawick, John
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US-10-282-122A-35107
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                                                                       APPLICANT: Trawlck, John D.
APPLICANT: Cart, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Devkaryotes
FILE REFRENCE: ELTTRA.011A
FILING PAPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 00/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
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Pred. No. 3.8e-81;
0; Mismatches 247;
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                                                         Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 73.4%;
Matches 680; Conservative (
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Rati L.
APPLICANT: Aplicant, Jouith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Apli, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Gen
TITLE OF INVENTION: Prockaryoues
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: 08/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
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ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35107
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Patent No. US20020061569A1
GENERAL INFORMATION:
SOFTWARE: Patentin version 3.1
SEQ ID NO 35107
LENGTH: 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 catadeadargrtageadacataagaaaarcaaarcagaartaageaaaartgereegae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 265.6; DB 9;
Pred. No. 8.2e-36;
0; Mismatches 354;
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22-25
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 8024
                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                      26.3%;
ilarity 57.8%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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US-09-815-242-8024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        494;
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Best Local
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Sequence 301, Application US/10470048B
Sequence 301, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: Patentin version 3.1
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                                         411 AATCATGTTAGTGGGGGGGGGGTTATAATGCAAATATTGATGCATTTAAAAGAGT
                                                                                             TTCAAAAGCTTTTAGGTAAAGAAGAAGGTAAAAAAACGCTTAGAAGAACACGATAAGAA
GATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAAACAAT
                                                                                                                                              471 cectalalecagiadecaladealadaladadecealadadecinegaladadente
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US-10-470-048B-301
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                                              879 TAAGTGGTTGAAATCAAGGGGTATTATCGCAAGTGAAGTATGGCAGAAGATTTAGAAAA 938
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          912 CTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAAATGGCAAAAGAACTTGTTGA
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tanicl Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tanimoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICANTON NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 264.6; DB 9; Length
Pred. No. 1.2e-35;
0; Mismatches 354; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILLING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-02-3
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SERICTH: 957
                                                                                                                                                                                                                                                                               Sequence 4194, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4194
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Best Local Similarity 57.8%
Matches 493; Conservative
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48 ATTGTTTGTTTTAATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGTAA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AGATAAGATTGGGGCATATGAATCGGTTGGATCTAGACCGCAACGAATATGGAAGTGAT 320
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                                   in Microorganisms
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorgani; FILE REFERENCE: ELITRA.014A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-66
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-12-20
PRIOR PELING DATE: 2001-12-20
PRIOR PELING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
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Pred. No. 2.1e-35;
0; Mismatches 408;
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Matches 524; Conservative C
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                                     TGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAAAATCGTATTAATAAACCATTAAG
                                                                                                                                                                  TATGAAACCTGTTGGTATTGCAGATGATGGCAGCACTAAAAATATAAAAAGTCAGTAAG
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Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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Pred. No.

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Best Local Similarity 74.89
Matches 279; Conservative
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                    621 TACATTTATGGGACAATTCTTAATTAAATGGGTATTCAACCTGAAGTCACAAAAGACAA 680
                                                                                                                                                            708 TACTAAAGGITIAAGIAAGIATCITAAAGGACCITACITACAAAIGAACACIGAAACTIT 767
                                                                                                                                                                                                                                 741 TGCCAATATCAATCCAAAAGTTATGATTTTAGCCACTGACGGAAAAACGGACAAAAA--- 797
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                                                                                                                                                                                                                                                                                                                                                                         888 ACGTGTTGATATTTTAGACCGTGACTTATGGCCAAGATCACGTGGTTTAATTTCTTCAGA 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 355, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                        561 GTTAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTTATTAATAATGAAGA
                                                                                          648 CTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGT
                                                                                                                                                                                                                                                                                                       828 TTCACTAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.1%; Score 222.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEFOME: (301) 309-8514
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Length 668;

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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                           998
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                                                                                             1 TTATTAGCACATCCAACTATTCATATGTTGGACAATTTTTAAACGAACTAGGATTTAA 60
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                                                                                                                                                          AGAAGCATTAAGTGATGATGTTACTAAAGGTTTAAGTAATTCTTAAAGGACCTTACTT
                                                                                                                                                                                                           <u>aaargcattaagtgacgatgtaacaaaaggtttaagtaaatatttgaaaggaccttactt</u>
                                                    TTTGCTTGCTCATCCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA
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ZIP: 20850
COMPUTER REABELE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
  Indels
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
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REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PlD1
TELECOMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 355, Application US/10329624
Publication No. US;20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
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STATE: Maryland
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| Publication No. US20030054436A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT:
| TILLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
| CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
| CITY: Rockville | STATE: Maryland | COUNTRY: USA
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPRRATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCIL Text
                                                                                                                                                                                                    22.1%; Score 222.6; DB 1
74.8%; Pred. No. 1.6e-28;
iive 0; Mismatches 94
                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 355: US-10-329-624-355
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TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ATTORNEY AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                         Best Local Similarity
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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                    Score 162.2; DB 8;
Pred. No. 2.3e-18;
0; Mismatches 50;
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FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/099,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2556, Application US/10329624 Publication No. US20040043037A1 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELERAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556: SEQUENCE CHARACTER.STICS:
LENGTH: 242 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                      Query Match 16.1%;
Best Local Similarity 79.3%;
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STATE: Maryland
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                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-781-986A-2556
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LENGTH: 897
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                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-32
PRIOR PLING DATE: 2000-05-32
PRIOR PLING DATE: 2000-05-36
PRIOR PLING DATE: 2000-05-36
PRIOR PLING DATE: 2000-05-36
PRIOR PLING DATE: 2000-05-36
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-09-36
PRIOR PLING DATE: 2000-09-36
PRIOR PLING DATE: 2000-09-36
PRIOR PLING DATE: 2000-09-36
                                                                                                                                                                                                                                                                                                                                   2 GATGCATTAGCAGCATTAGACGTTAAACCAGTTGGTATTGCTGATGATGGTAAGAAAAA
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                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                              Score 162.2; DB 1
Pred. No. 2.3e-18;
NAME: Mark J. Hyman
REGISTRATION UNDERE: 46,789
REFERENCE/DOCKET NUMBER: PB248PlD1
TELECOMMUNICATION INPORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                            TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 2556: US-10-329-624-2556
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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Malone, Cheryl
Haselbeck, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                               Best Local Similarity 79.3
Matches 191, Conservative
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US-10-282-122A-30706
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APPLICANT:
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423 ACAAAAATCGGTGATTTATTAGGTAAATCAAAAGAAATGCAAGCGCGTATTGCAAAACA 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 ATTCCTAAGTCAACTAGGTTTTAAAGAAGCATTAAGTGATGATGTTACTAAAGGTTTAAG 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              783 TGAGCGTATGTTCATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACT 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TCGTGATGAGAGTATTGCAAGAAATG 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  843 AGAAAAAGATCCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATATTTT 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAGCGGATGATAACAAAAAAATCGTATTATTAAACCATTAAGAGATAAAATTGGAAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 AGATTTGATCATTGCCGATGATAATCGCCATTCTGCCGTCTATGAAGAACTCAAAAAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTCCTACGATTGAACTGAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 TAAGCAGGATATTGCGG-----ACATCGCCAAAACGTTACCGAAAAGGGGAAAAAAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 critagiggaagrecriaddriarcaaargccaaaaagcccgridccaaraaccaaccraargc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 refrecerradaarafretrangredarecacrrecacaaarregrerecerefree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGTTGAAATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 TGTCGCAGATGACAATGATAAAACCCGTATTCTGCAAAAAGTACGCGATAAAGTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATACACTTCTGTAGGAACACGTAAGCAACCTAAACTTAGAAGAAATCAGTAAAACC
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                                                                                                                                                                                                                                                                               See File Wrapper or PALM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 156.4; DB Pred. No. 3.2e-17
                                                                                                                                                                                                                                                                           Remaining Prior Application data removed WINBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 30706
PRIOR APPLICATION NUMBER: 60/253,625
RRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
RRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pasteurella multocida
US-10-282-122A-30706
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Best Local Similarity 51.9%;
Matches 454; Conservative
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716 GITIBAGIBAGIBICITBAAGGACCITACITBCAAAIGAACACIGAAACTITBICICAAG 775
                                                            535 GCGATGCCGAAAACGGTGAATCCGTCAATATTAAAATGACGCTCGAACAGCTGCTTGAGA 594
                                                                                                                                                                                     595 pagarcccgacgriatrerccrgargacgagagagagagaraaagrcgargagacgga 654
                                                                                                                                                                                                                                                                                                                        655 AAAGACCGATCGAAAAGATCCTCTTTGGAAAAGCTCAGCGCAGTCAAAAACGGCAAGG 714
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CURRENT APPLICATION: Identification of EBSential Genes in Microorganisms
FILE REFERENCE: ELITAR, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/230,337

PRIOR APPLICATION NUMBER: 60/245,578

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

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PRIOR PLING DATE: 2001-02-06
                                                                                                                                                                                                                                                        TAAAAGAACTAGAAAAAGATCCTGTATGGAAGAAATTAAAACGCTGTGAAAAATCAACGTG
                                                                                                                            776 TGAATCCTGAGCGTATGTTCATAATGAC---AAACAAAGCAAGTTCTAACGAACCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 143.2; DB 17; Length 972; Pred. No. 5.7e-15;
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Sequence 9415, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:
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SEQ ID NO 9415
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US-10-282-122A-9415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
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Forsyth, R.
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Best Local Similarity
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                                               176 AACGTGTTGTTGTTCTTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAAC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTCGGAATTGCGGACGACGCAAACCTAAGTTTATTAACGAGAAAGGTCAGGGGAAAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536 AAGAACACGATAAGAAATTGAAGAATATAAAAAAGAAATAACTATGGATAAAATCAAA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 CTGAACATAAACAAAAGCTGGATGAATTGAAACAGAAATTCGGCAGCCGGAAACAGAGCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 TTCTTCTGGTGGGAACACAATGAAGAATCACCGTGCGCGATGAA---AACTTTTTCA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     656 TIGGICAAITCCTAAGICAACTAGGITITIAAAGAAGCAITAAGIGAIGAIGTITACTAAAG 715
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          903 AGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAATGGCAAAAGA
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                                                                                                                                                                                                                                                                                                                                                   Sequence 2066, Application US/09974300
| Patent No. US20020146721A1
| GENERAL INPORMATION:
| APPLICANT: Berka, Randy M. |
| APPLICANT: Clausen, ID Groth | TITLE OF INVENTION: Machods For Monitoring Multiple Gene | TITLE OF INVENTION: DEADERSON | FILE REFERENCE: 10085.500-US | CURRENT APPLICATION WUMBER: US/09/974,300 | CURRENT APPLICATION NUMBER: 09/680,598 | PRIOR FILING DATE: 2001-10-05 | PRIOR APPLICATION NUMBER: 09/680,598 | PRIOR PLILING DATE: 2001-10-06 | PRIOR PLILING DATE: 2001-10-06 | PRIOR PLILING DATE: 2001-3-27 | NUMBER OF SEQ ID NOS: 8481 | SOCTWARE: PRESENCE for Windows Version 4.0 | SEQ ID NO 2066 | LENGTH: 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 4.8e-16;
0; Mismatches 376;
                                                                                                                                      963 ACTTGTTGAATTATCTAAGAAAGATAGTAAAAAA 996
                                                                                                                                                                                                   864 AGTCCAAGACTTTGTAACGAAATCCGCCAAATAA 897

    TYPE: DNA
    ORGANISM: Bacillus licheniformis
US-09-974-300-2066

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Best Local Similarity 51.8%;
Matches 414; Conservative
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US-09-974-300-2066
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US-10-282-122A-4605/c
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                                                                                                                                                                                                     67 GAGGAGAAAAAAAAAAAAAAGCGGACAATAAAAATCAAGCTATAAACAATTAAACACCT 126
                                                                                                                                                                                                                                                                                                            127 gaagggaaacgaagtragaraaaccagcgaaaaagragrigracrigaargggtarar 186
                                                                                                                                                                                                                                                                                                                                                                205 GTTGATGCGTTAGTTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAAAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                 187 rcagaagacrirarragcacrirgsrgrircagccagragggarggcagacarraagaarrar 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AATCGTATTATAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 AATAAATGGGTAAATACAAAAACAAAACCGAGTAAAGATGTTGTAGATGTCGGGACACGT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 AATAGACACAAAGGTATTTATAAAGACTTAAATAAATTGCTCCTACGAT-----T 435
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                                                   25 AAAATTTTAAGTGTAATTGGCTTATTGTTTTTAATTGCAACTGCAGCATGTGGAAAT 84
                                                                                                 7 AAAATICCICAGIATITICATAGIAGITITICIATICGCIGITGGATGCGGACAGCAAAA 66
                                                                                                                                                                                                                                                            GAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTGTTGTTGAGTATTCATTT
  Gaps
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APPLICANT: Oblean, Kari L.

APPLICANT: Zyekind, Judith W.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Cart, Grant J.

APPLICANT: Vamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

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APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Prokaryotes

FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
0; Mismatches 243; Indels
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 GAAGAATATAAAAAAAAAT 575
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     Matches 308; Conservative
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US-09-815-242-2107/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 GGTTGGATCTAGACCGCAACGAATATGGAAGTGATAAGTAAATTAAAACCGGATTTGAT 32
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Pred. No. 1.7e-12;
0; Mismatches 85
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SSCTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2107
LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 TATTGCTGATAATAATAGACACAA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carrecagarerrageagacaraa
                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-2107
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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Best Local Similarity 67.8%;
Matches 179; Conservative
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Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 604, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynuclectides and Sequences
NUMBER OF SEQUENCES: 5.255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 TGATGGCAGCACTAAAAATATAACAAAGTCAGTAAGAGATAAGATTGGGGCATATGAATC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 AATCAAGCACGAAGAAGGTACTACGAAAGTACCTAAACACCCTAAACGTGTTGTTCT
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                                                                                                                                                                                                                                                             Gaps
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFFWARE: Patentin version 3.1
SEQ ID NO 4605
LENGTH: 321
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                                                                                                                                                                                                                      Length 321;
                                                                                                                                                                                                                                                           0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP VECTER 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
                                                                                                                                                                                                                      Score 128; DB 17;
Pred. No. 1.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 TATTGCTGATAATAATAGACACAA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ 1D NO: 604:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 CATTGCAGATGTTAGCAGACATAA
                                                                                                                                                                 ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.8%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                  US-10-282-122A-4605
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US-08-781-986A-604
                                                                                                                                                    TYPE: DNA
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APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 ACAAAAA-----TAGAACGAAATICATTGATCCTGCAGITTGGAAATCATTAAAAGCTG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                698 GTGATGATGTTACTAAAGGTTTAAGTAAGTATCTTAAAGGACCTTACTACAAATGAACA
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                                                                                                                                                                                                     . 9
                                                                                                                                                     Length 2115;
                                                                                                                                                  Score 125.4; DB 8; Length
Pred. No. 7.5e-12;
1; Mismatches 247; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 604, Application US/10329624 Publication No. US20040043037Al GENERAL INFORMATION:
                                                                                                                                                     h
Similarity 53.2%;
LENGTH: 2115 base pairs
                                                                                                                                                                             Best Local Similarity 53.2
Matches 289; Conservative
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STATE: Maryland
                             TYPE: nucleic acid
STRANDEDNESS: double
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                             ; TYPE: nucleic aci
; STRANDEDNESS: dov
; TOPOLOGY: linear
US-08-781-986A-604
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                                                                                                                                                        Query Match
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US-10-470-048B-318
                                                                                                                                                                       SEQ ID NO 318
LENGTH: 990
                                                                                                                                                                                                 TYPE: DNA
ORGANISM: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878 TGAAAAATCAACGTGTTGATATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAA 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 AAGGTAAAAAACGCTTAGAAGAACACGATAAGAAAATTGAAGAATATAAAAAAGAAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ATAATGAAGATACATTTATGGGACAATTCTTAATTAAATGGGTATTCAACCTGAAGTCA
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                                                                                                                                                                                                                                                                                                                                                                Score 125.4; DB 18;
Pred. No. 7.5e-12;
1; Mismatches 247;
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                       NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PlD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
WATION FOR SEQ ID NO: 604:
                                               APPLICATION NUMBER: US/10/329,624 FILING DATE: 27-Dec-2002 PRIOR APPLICATION DATA:
                                                                                  APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 604: 08-10-329-624-604
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid STRANDEDNESS: double
                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.2%;
Matches 289; Conservative
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                                                                                        APPLICATE: MEINTE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
SOFTWARE: PATENTING DATE: 2003-07-25
SOFTWARE: PATENTIN OFS: 603
SOFTWARE: PATENTIN OFS: 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124; DB 21;
Pred. No. 1.1e-11;
0; Mismatches 380;
Sequence 318, Application US/10470048B Publication No. US20050037444A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORGANISM: Staphylococcus aureus US-10-470-048B-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.7%;
Matches 412; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743
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TTCAAATAAACAATCATCAGATAACAAAGATAAGGAAACAACTTCAATTAAACATGCAAT 137
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                 185 GGAAAGAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAGTAGCTGCATTCC
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                                                                                                                                                                                                                                                              662 ATTTAGGATTCAAACGTAATAAAGACTTACAAAAACAAGTTGATAATGGTAAAAGATATTA
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                                                                     AAAAAGA----AATAACTATGGATAAAAATCAAAAGGTATTGCCTGCAGTAGCTGCTAAAT
                                                                                                                 545 AAAAAGATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAAGCTTCAGTTGTTAACT
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PB461USD2
CURRENT APPLICATION NUMBER: US/10/967,189
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 10/278,946
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 1902-01-15
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PRILING DATE: 1999-03-06
PRIOR FILING DATE: 1999-03-06
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50.7%; Pred. No. 1.1e-11;
tive 0; Mismatches 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/10967189; Publication No. US20050053995A1; GENERAL INFORMATION:
  ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-967-189-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.1
SEQ ID NO 15
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Matches 412; Conservative
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TAGTTCAAGTAACTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAAATCAAGCACGAAGA 146
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFRERENCE: P846/USD1
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/830,217
PRIOR PILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
PRIOR PILING DATE: 1099-03-18
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-04
PRIOR PILING DATE: 1998-04-04
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Version 3.1
SEQ ID NO 15
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                                                                            803 CAAACAAAGCAAGTTCTAACGAACCTTCACTA 834
                                                                                                                         776 AATCAGATCCAAATGCGAAAGATGCTGCATTA 807
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7 ORGANISM: Staphylococcus aureus
US-10-278-946-15
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Best Local Similarity 50.7%;
Matches 412; Conservative
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US-10-278-946-15
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APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland
                                                                                                             446
                                                                                                                                                                                                                                                                               622
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                                                    GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAA 386
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TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
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                                                                                                            TAGACACAAAGGTATTTATAAAGACTTAAATAAAATTGCTCCTACGATTGAACTGAAAAG
                                                                                                                                      378 TAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACC-----AACAG
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                        258 acceaaaticeaatacataaaaateattiaaaagatactaagatictagetcaagaace
                                                                                                                                                                  TITCGATGGAGATTATAATGAAAAT-ATTGATGCTTTTAAAACAATTTCAAAAGCTTTAG
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ZIDS 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
US-08-781-986A-238
; Sequence 238, Application US/08781986A
; Publication No. US20030054436A1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTAAAATGCTTGTTGCTTTGCCTTTCCTACTTGTTTTAGCAGGATGTAGTGGGAA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGTATTATTAAACCATTAAGAGATAAAATTGGAAAATACACTTCTGTAGGAACACGTAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 accgaarricgaaracaraaaaaaargarriaaaagaracraagarrigraggroaagaacc 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reacgregratarciitiagestataaaccigiaggrecigiagaatcaiggacacaaaa
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                                                                                                                                                                                                                                                                                                                          Length 3775;
                                                                                                                                                                                                                                                                                                                    Score 124; DB 8; Length 37
Pred. No. 1.5e-11;
0; Mismatches 380; Indels
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TELECOMMUNICATION INFORMATION:
                              TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 238
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.7%;
Matches 412; Conservative
                                                                                                                                               3775 base pairs
                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-781-986A-238
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446 466 505 703

742

622 646 682

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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR, 0.34

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27
                             GCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTATTGCTGATAATAA 386
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                                                                                             360 TGCACCTAACTTAGAGGAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCAAAAGT
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Ohlsen, Kari
Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rdacorcororateritradororraakocióradororroradaarcarogacadaaa 299
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12.3%; Score 124; DB 18; Length 3775;
Best Local Similarity 50.7%; Pred. No. 1.5e-11;
Matches 412; Conservative 0; Mismatches 380; Indels 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIORICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION CONTROL FEB PE348PID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 238: US-10-329-624-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
                      Sequence 238, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-8439
INPORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
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STRANDEDNESS: double
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US-10-329-624-238
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                                                                                                                                                                                                                                                                                                                                                            191 TTGAGTATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                 2 TIGAAIGGGTATATICAGAAGACTTATIAGCACTIGGTGTTCAGCCAGTAGGGAIGGCAG
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                                                                                                                                                                                                                                                                                   Length 796
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                   DB 17;
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PRIOR APPLICATION NUMBER: 60/25/25
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
Remaining Prior Application data removed - S
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10009
                                                                                                                                                                                                                                                                                   Score 113.2;
Pred. No. 7e-
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19870, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                Query Match
11.2%;
Best Local Similarity 57.6%;
Matches 227; Conservative
                                                                                                                                                                                                                            ; ORGANISM: Bacillus anthracis
US-10-282-122A-10009
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Carr, Grant
Yamamoto, Robert
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Trawick, Joh
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APPLICANT:
APPLICANT:
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                                                                    PRIOR FILING DATE: 2000-09-06
PRIOR PRILAY JATE: 2000-09-06
PRIOR PELITAG DATE: 2000-09-06
PRIOR PLILAG DATE: 2000-09-06
PRIOR PLILAG DATE: 2000-09-09
PRIOR PLILAG DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRILAG DATE: 2000-11-27
PRIOR PRILAG DATE: 2000-11-27
PRIOR PLILAG DATE: 2000-11-27
PRIOR PLILAG DATE: 2000-11-27
PRIOR PLILAG DATE: 2001-02-09
PRIOR PLILAG DATE: 2001-02-09
PRIOR PLILAG DATE: 2001-02-09
PRIOR PLILAG DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-06
PRIOR PRILAG DATE: 2001-02-16
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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60/207,727
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Zyskind, Judith W.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Rari
APPLICANT: Wall, Sykind, Judith
APPLICANT: Wall, Daniel
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Matches 217; Conservative
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APPLICANT: FORSEYT, R. APPLICANT: APPLICANT: ALL MAPPLICANT: ALL MAPPLICANT: You, H. APPLICANT: Xu, H. APPLICANT: Xu, H. Identification of Essential Genes in Microorganisms of TITE OF INVENTION: ELITRA.034A CURRENT FILING DATE: 2003-20-20

PRIOR APPLICATION NUMBER: 60/1204

PRIOR APPLICATION NUMBER: 60/1204

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 ATTCATTTGTTGATGCGTTAGTTGCTTTAGATGTTAAAACCTGTTGGGATAGCGGATGATA
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                                                                                                                                                                                                                                                                                                                                                  Length 10244;
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                                                      APPLICANT: Levy, Stuart, et. al.
TITLE OF INVENTION: NIMR COMPOSITIONS AND THEIR METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                  Score 95.2; DB 21;
Pred. No. 1.6e-06;
0; Mismatches 203;
                                                                             TITLE OF INVENTACE: PEZ-043
CURRENT APPLICATION NUMBER: US/10/893,671
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US/09/801,563
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
SEQ ID NO 14
LENGTH: 10244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17083, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
Sequence 14, Application US/10893671
Publication No. US20050064527A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                      Query Match

9.4%;

Best Local Similarity 51.7%;

Matches 217; Conservative
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Forsyth, R.
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US-10-893-671-14
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Carr, Grant
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APPLICANT:
APPLICANT:
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Pred. No. 0.00049;
PRIOR APLILAGATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
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Similarity 47.1%;
12; Conservative (
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SEQ ID NO 17083
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Sequence 5558, Application US/09960352
Sequence 5558, Application US/09960352
Sequence 5558, Application US/09960352
Sequence 5558, Application
GENERAL INFORMATION:
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, NaCLER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF SEQ ID NOS: 15112
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5558
LENGTH: 431
198 TCAAGGCACCACTGAGATCCCTGCTCACCACAAAAAGTGGTTGTGATGAACATGGAAAA 257
                                                                                                                                                                                                                                                                                                                                                                     378 GTTTGAACCAAACTACGAAAACTCAGTACTACTGCCCCTGATCTGATTTTAACGGGTAG 437
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                                                                                       204 TGTTGATGCGTTAGTTGCTTTAGATGTTAAACCTGTTGGGATAGCGGATGATAACAAAA
                                                                                                                                            Gaps
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; OTHER INFORMATION: Clone ID: 24-LIB3057-024-Q1-K1-F7
US-09-960-352-5558
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Pred. No.
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Best Local Similarity 51.4%;
Matches 180; Conservative (
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US-09-960-352-5558/c
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-24
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-06
PRIOR PELLING DATE: 2000-09-06
PRIOR PELLING DATE: 2000-09-09
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PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
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PRIOR PELLING DATE: 2001-12-22
PRIOR PELLING DATE: 2001-12-22
PRIOR PELLING DATE: 2001-02-06
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                                                                                          612 Trraagigratriggraagaarcaagarriagrararraraaragarrirgaarrirga 671
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                                      TITGCTTGCTCAACCAAGCAACTCTTATGTTGGTCAATTCCTAAGTCAACTAGGTTTTAA
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                             ; Sequence 32601, Application US/10282122A
; Publication No. US20040029129Al
; GENERAL INFORMATION:
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SEQ ID NO 32601
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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Best Local Similarity
Matches 271; Conserv
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APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21/522741B
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 6774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ACCAGATTTAATTATTGCTGATAATAATAGACACAAAGGTATTTATAAAGACTTAAATAA 419
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553
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CAAAAGCTTTAGGTAAAGAAGAAGAAGGTAAAAAACGCTTAGAAGAACACACGATAAGAAAA
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                                                                                            Indels
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49.3%; Pred. No. 0.00065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(478)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-010-Q1-N6-E1
US-10-021-323-6774
                                                                                                                                                                               Sequence 6774, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, J111
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NAME/KEY: unsure
LOCATION: (1)..(4
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APPLICANT: Foreyth, R.
APPLICANT: Foreyth, R.
APPLICANT: Yu, H.
TITIE OF INVENTION: Identification of Essential Genes in Microorganisms FILIE DEFINATION: Identification of Essential Genes in Microorganisms FILIE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/291,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
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PRIOR FILING DATE: 2000-12-22
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PRIOR PILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 0.0017;
0; Mismatches 242;
Sequence 33236, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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US-10-282-122A-33236
                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
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Forsyth, R.
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Best Local Similarity 47.74
Matches 221; Conservative
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SEQ ID NO 33236
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RESULT 36 US-10-282-122A-33236

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Sequence 120013, Application US/10425115
| Sequence 120013, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Kovalic, David K.
| APPLICANT: ADOI, Yihua
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Numbers US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT PILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 120013
| LENGTH: 1062
                                                                                                                                                              799 далатададададададададададададададататадададададададададададада 740
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                                                                                                                       795 CATAATGACAAACAAAGCAAGTTCTAACGAACCTTCACTAAAAGAACTAGAAAAAGATCC
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                                                                                314 TAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAACCAGATTTAATTA
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Pred. No. 0.0033;
0; Mismatches 168; Indels 0;
                                                                                                                                                                                                          855 TGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGATA 898
                                                                                                                                                                                                                                                 489 ACTACATAATAGATCAAAAAAACCAAACATACAAAACCTGATA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 TTGAAGAATATAAAAAAGAAATAACTATGGATAAAAATCAAAA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: MRT4577_40935C.1
US-10-425-115-120013
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OTHER INFORMATION: unsure at all n locations
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Best Local Similarity 51.0%;
Matches 175; Conservative (
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ORGANISM: Zea mays
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US-10-424-599-102083
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Publication No. US20040214272A1
Sequence 115706, Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rose, Thomas J.
APPLICANT: APPLICANT: About Yihua
APPLICANT: Cao, Yongue
APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 115706
LENGTH: 1121
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                                                                                                      413 TGATCGGCATGGCGCTGGGCAAAGGCCCCGGAGATGCAGGCGCGAAATCGCAGAAAAACCGTC 472
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                                                                                                                                               548 AGAAATTGAAGAATATAAAAAGAAATAACTATGGATAAAAA 590
                                                                                                                                                                                      173 AGCACCTGAAAACCGTTGCCGAGCAGATTCCTGCCGACAGCAA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Clone ID: MRT4577_37006C.1
U8-10-425-115-115706
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OTHER INFORMATION: unsure at all n locations
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Best Local Similarity
Matches 288; Conserva
                                                                                                                                                                                                                                                     RESULT 37
US-10-425-115-115706/c
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NAME/KEY: unsure
LOCATION: (1)..(1243)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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Best Local Similarity
Matches 330; Conserva
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| Sequence 172717, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cavalic, David K.
| APPLICANT: Zhou, Yihua
| APPLICANT: Cao, Yongweil
| APPLICANT: Cao, Yongweil
| APPLICANT: Cao, Yongweil
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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| TITLE REPERRICE: 38-21(5322)
| TITLE REPERRICE: 
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Pred. No. 0.0037;
0; Mismatches 176; Indels
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US-10-424-599-102083
Sequence 102083, Application US/10424599; Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof for P
FILE REFERENCE: 38-21(532318
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(1214)
OTHER INFORMATION: unsure at all n locations
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Best Local Similarity 48.7%;
Matches 167; Conservative
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US-10-425-115-172717/c
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                                                            Length 1243;
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                                                              DB 20;
0.0037;
; OTHER INFORMATION: Clone ID: MRT4577_89100C.1
US-10-425-115-172717
                                                              Score 74;
Pred. No.
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ilarity 43.7%;
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